

Integrating Distributed Information: The ToolBus/PathPort System

Dr. J Dana Eckart
Virginia Bioinformatics Institute
<https://www.vbi.vt.edu>



What is ToolBus/PathPort?

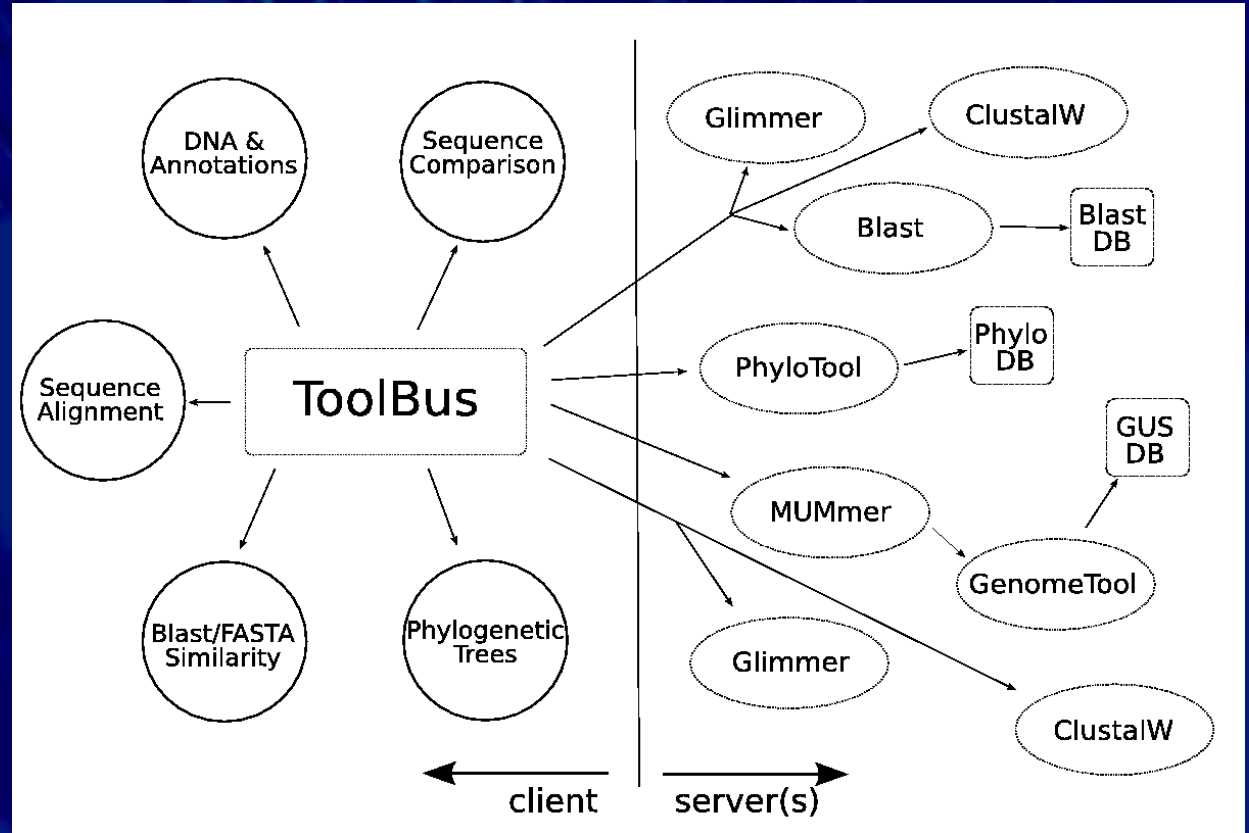
Platform Neutral

Utilizes SOA

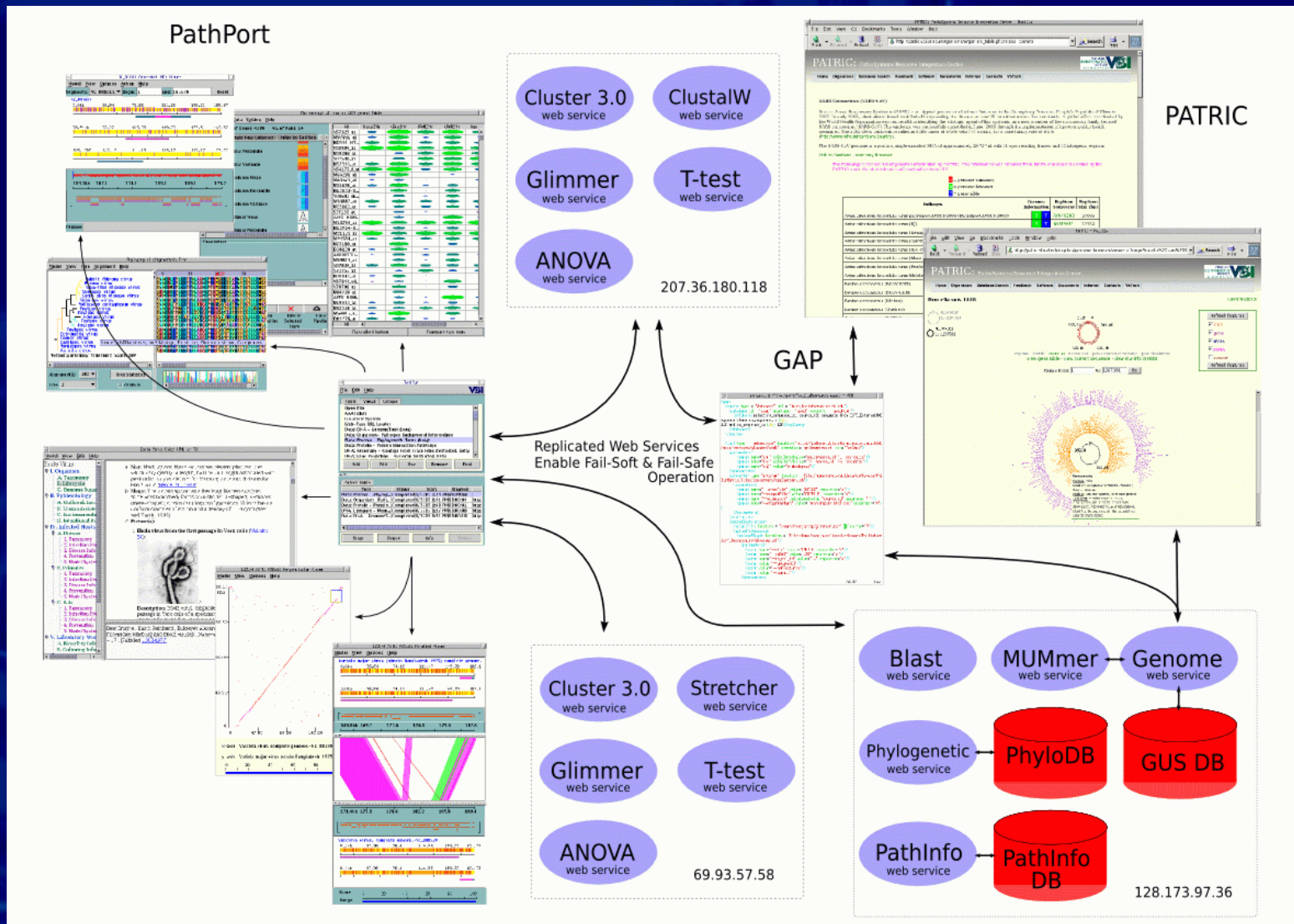
Visual plugins

Fail Soft/Safe

Data Integrator



Putting It All Together



Comparing Vaccinia & Variola

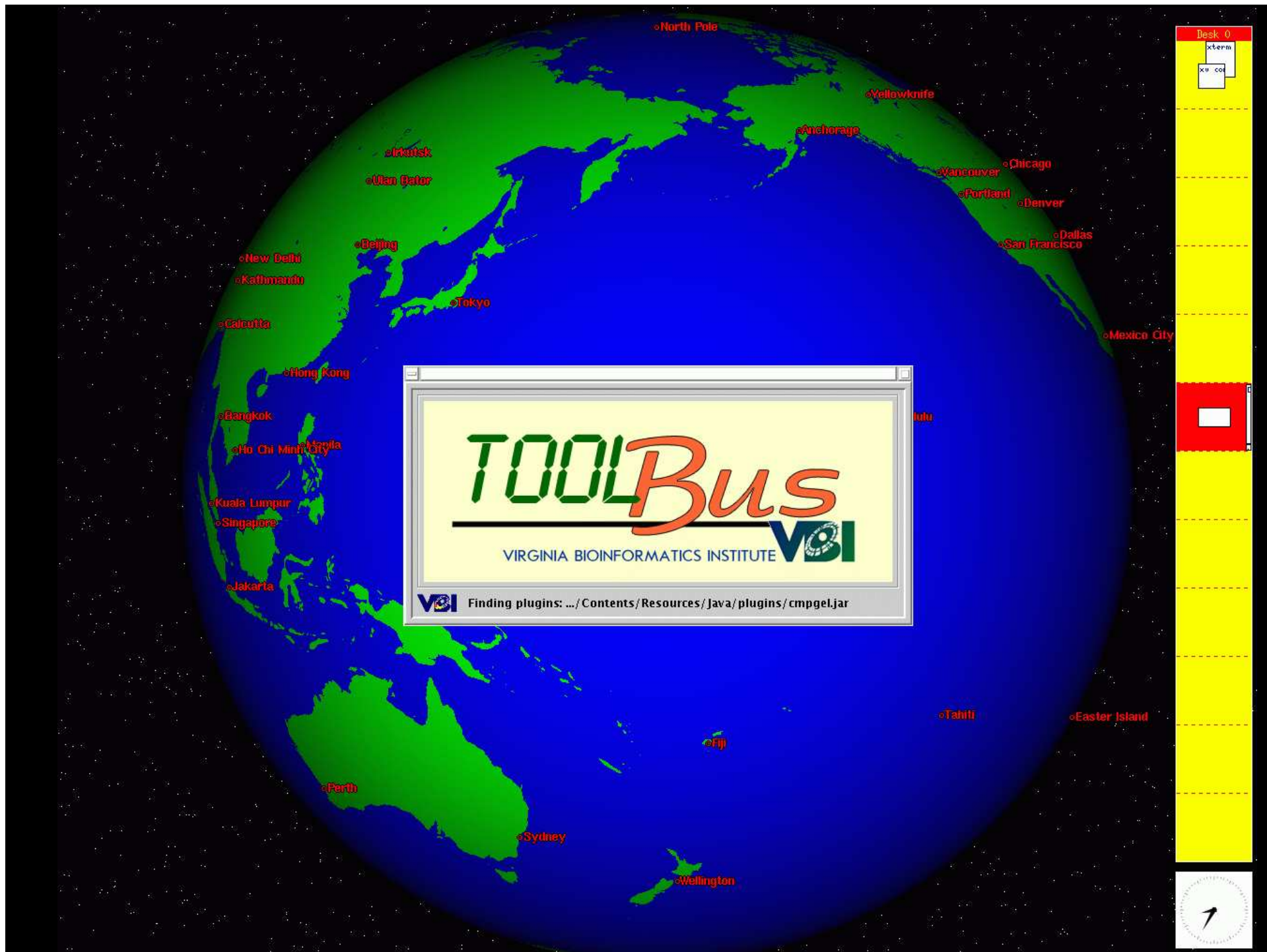
MUMmer comparison

Blast search

ClustalW alignment

Phylogenetic analysis

Pathogen Information



ToolBus

File Edit Help

Tools Views Groups

Open File
AAATicket
Local File System
Web-Page URL Loader
Data: DNA - GenomeTool (beta)
Data: Organism- Pathogen Background Information
Data: Protein - Phylogenetic Trees (beta)
Data: Protein - Protein Interaction Pathways
DNA: Assembly - Contigs From Trace Files (restricted, beta)
DNA: Gene Prediction - Genscan (restricted, beta)
DNA: Gene Prediction - Glimmer (beta)
DNA: Gene Prediction - BDGF (restricted, beta)
DNA: Gene Prediction - GlimmerM (beta)

Add Edit Use Remove

Active Tools

Tool	Status	Start	End
DNA: Compare - Mum...	Initialize		

Stop Reuse Info

Use DNA: Compare - Mummer (beta)

DNA: Compare - Mummer (beta)

Maximum unique matches for doing large sequence comparisons.

mummerFiles mummerFileAndAnnotations

mummerAnnotations_Basic mummerAnnotations_Advanced

MUMs MUMmer output - MUMs or Extended MUMs

Abelson murine leukemia virus, complete genome.\$NC_0014 Name of file

Start position of first (reference) segment (leave blank for default)

End position of first (reference) segment (leave blank for default)

No annotations Type of annotation

Abelson murine leukemia virus, complete genome.\$NC_0014 Name of sequence

Start position of second (query) segment (leave blank for default)

End position of second (query) segment (leave blank for default)

No annotations Type of annotation

Run Reset About Cancel

Desk 0

Use DN

ToolB

Use DN



ToolBus

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Maximum unique matches for doing large sequence comparisons.

mummerFiles mummerFileAndAnnotations

mummerAnnotations_Basic mummerAnnotations_Advanced

Extended MUMs MUMmer output - MUMs or Extended MUMs

Vaccinia virus, complete genome.\$NC_001559\$1 Name of file

Start position of first (reference) segment (leave blank for default)

End position of first (reference) segment (leave blank for default)

Minimal annotations Type of annotation

Varola major virus (strain Bangladesh-1975) complete genome Name of sequence

Start position of second (query) segment (leave blank for default)

End position of second (query) segment (leave blank for default)

Minimal annotations Type of annotation


Run Reset About Cancel

Desk 0

Use DN

TooIB

Use DN



ToolBus

File Edit Help

Tools Views Groups

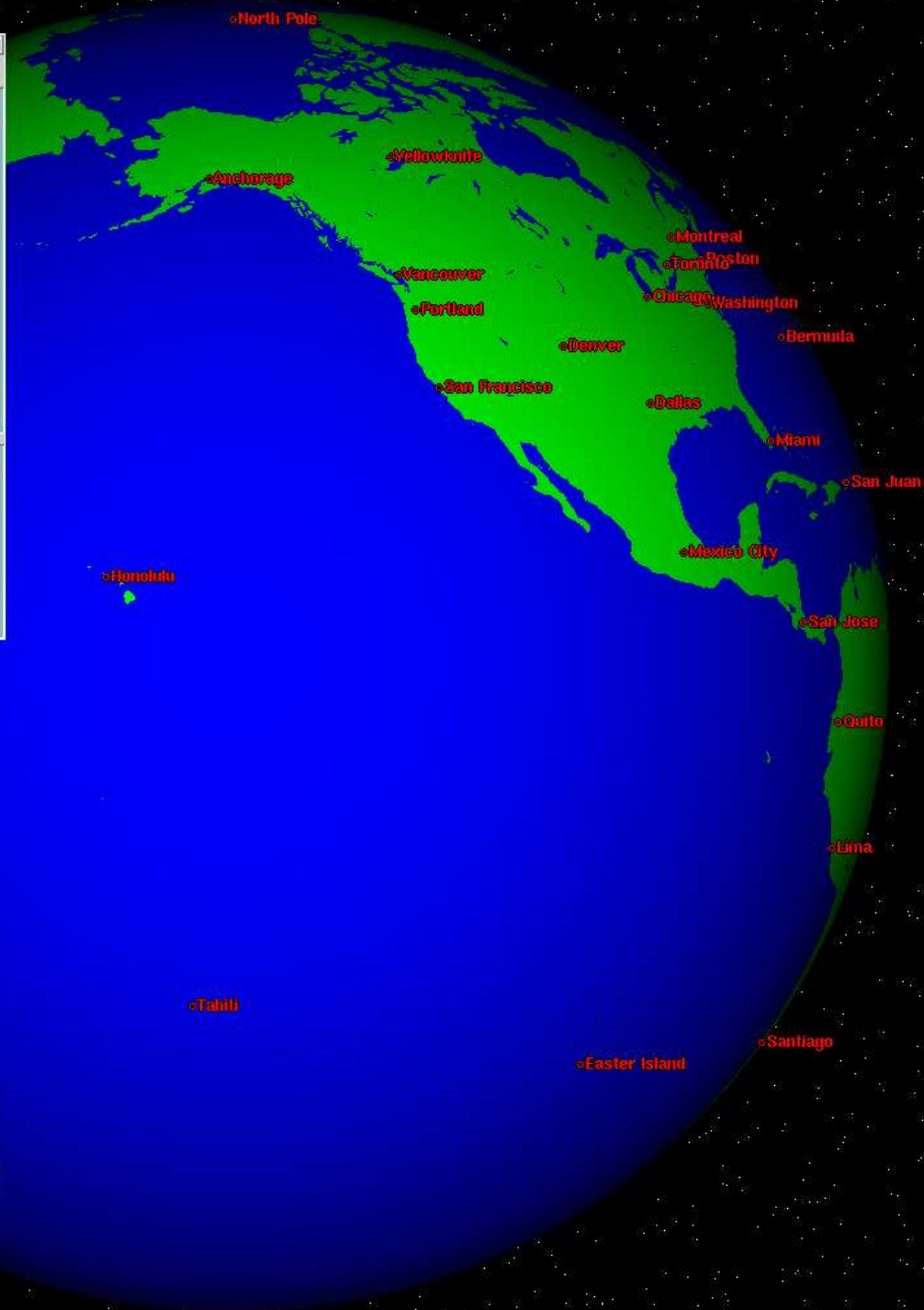
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DNA: Gene Prediction - GlimmerM (beta)

Add Edit Use Remove Find

Active Tools

Tool	Status	Start	Elapsed
DNA: Compare - Mum...	Running	4/29/05 5:44 ...	00:00:08

Stop Reuse Info Delete



Desk 0

xv co

ToolB

ToolBus

File Edit Help

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DNA: Gene Prediction - GlimmerM (beta)

Add Edit Use Remove Find

Active Tools

Tool	Status	Start	Elapsed
DNA: Compare - Mum...	Completed	4/29/05 5:44 ...	00:00:17 http...

Stop Reuse Info Delete

New data from DNA: Compare - Mummer (beta)

Model(s) to Create

Sequence Comparison
Generic XML

Save Data to File

Browse

External App/Web Browser

Find

☐ Web Browser

OK Cancel

Desk 0

XV CO

ToolBus

New

Compass

ToolBus

File Edit Help

Tools Views Groups

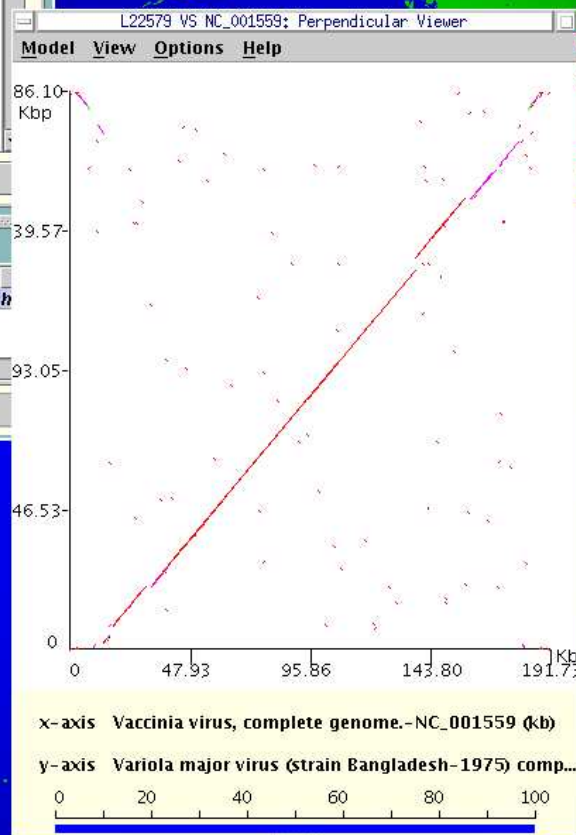
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Add Edit Use Remove Find

Active Tools

Tool	Status	Start	Elapsed
DNA: Compare - Mum...	Completed	4/29/05 5:44 ...	00:00:17 h

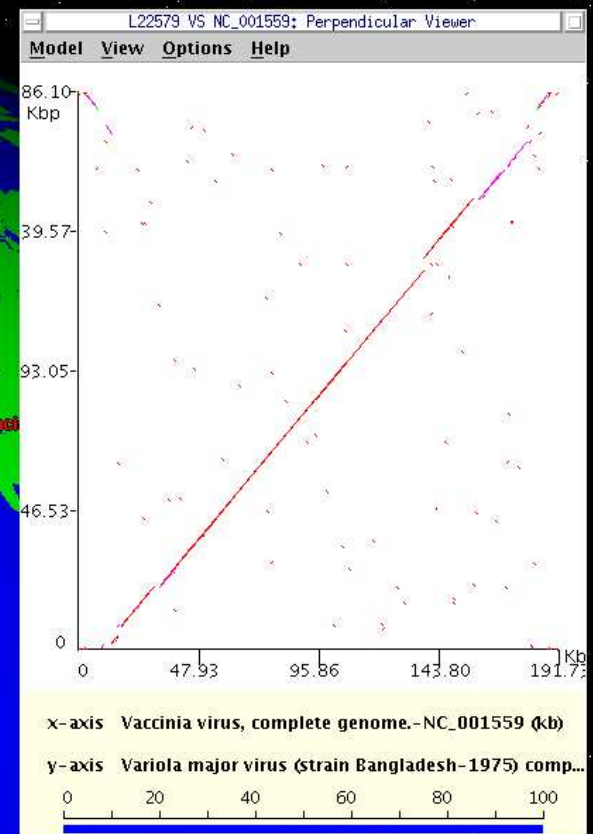
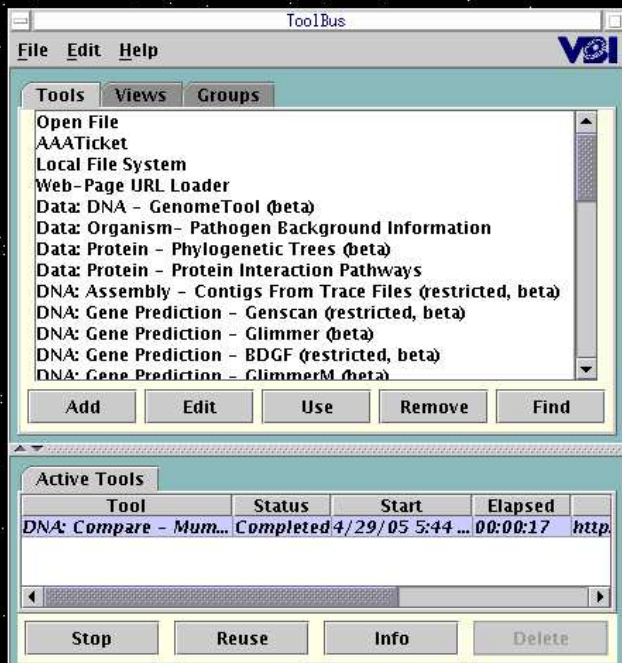
Stop Reuse Info Delete



Desk 0

xx co

ToolB L2257



Sydney

Fiji

Tahiti

Wellington

Easter Island

Santiago

Lima



ToolBus

File Edit Help

Tools Views Groups

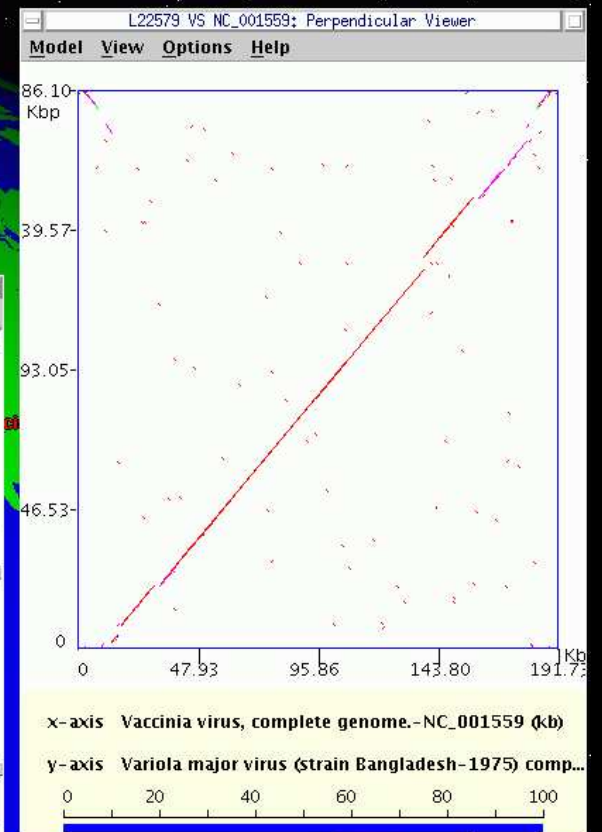
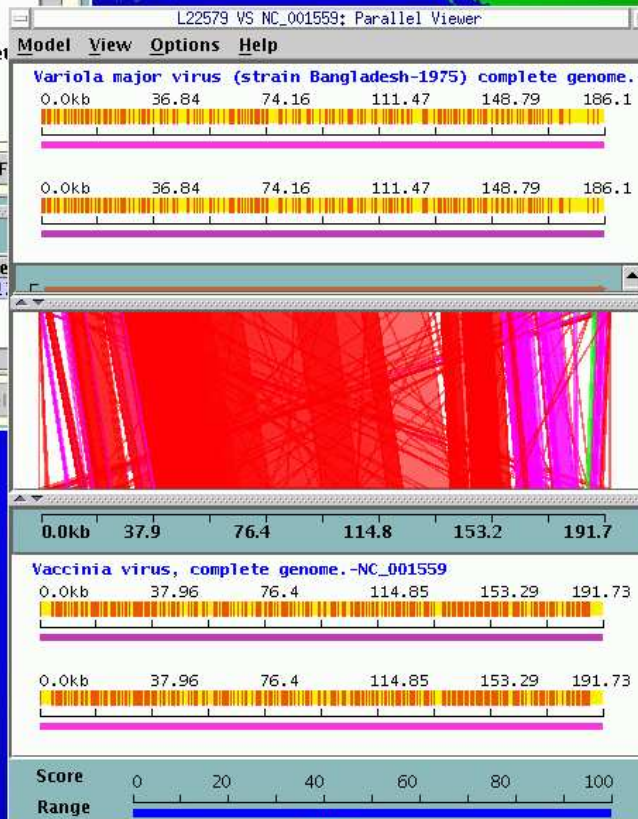
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Add Edit Use Remove

Active Tools

Tool	Status	Start	Elapse
DNA: Compare - Mum...	Completed	4/29/05 5:44 ...	00:00:1...

Stop Reuse Info Del



Fiji

Sydney

Wellington

London

Easter Island

Santiago

Lima



ToolBus

File Edit Help

Tools Views Groups

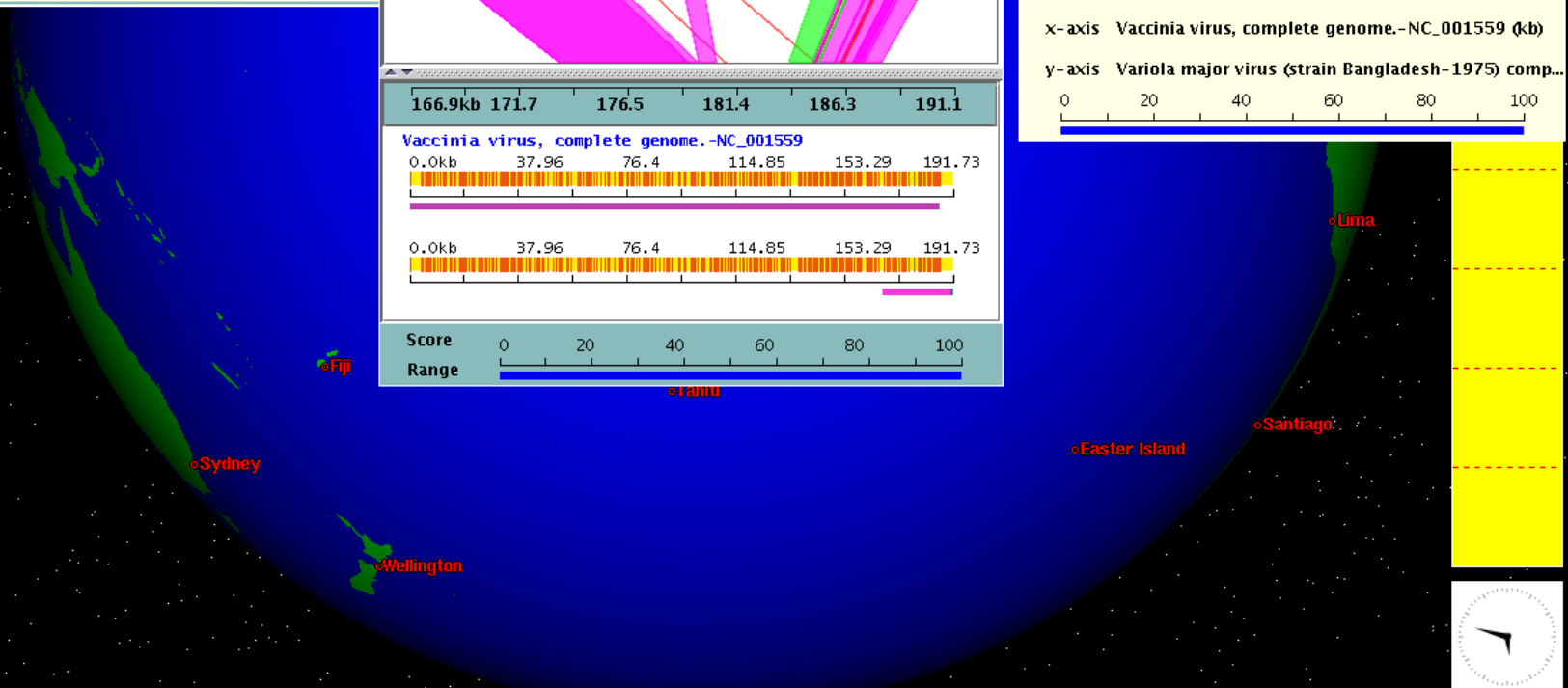
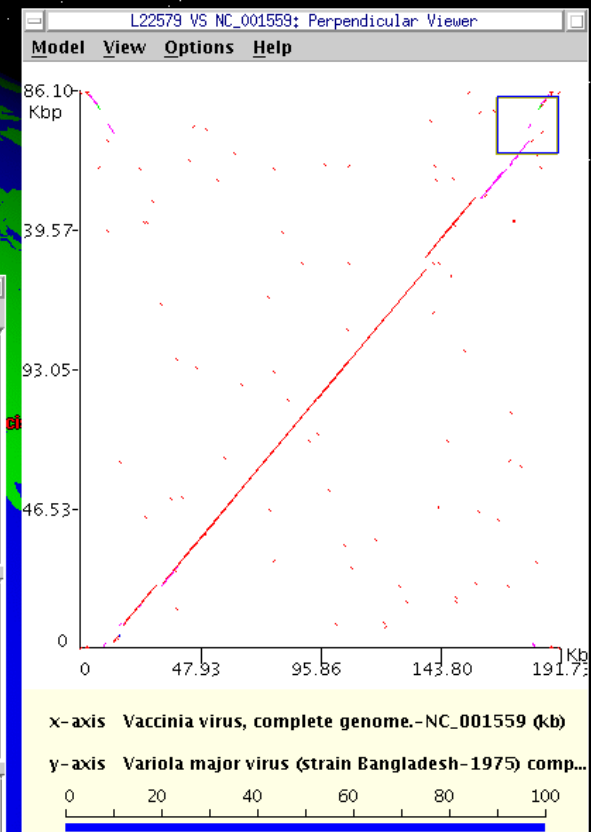
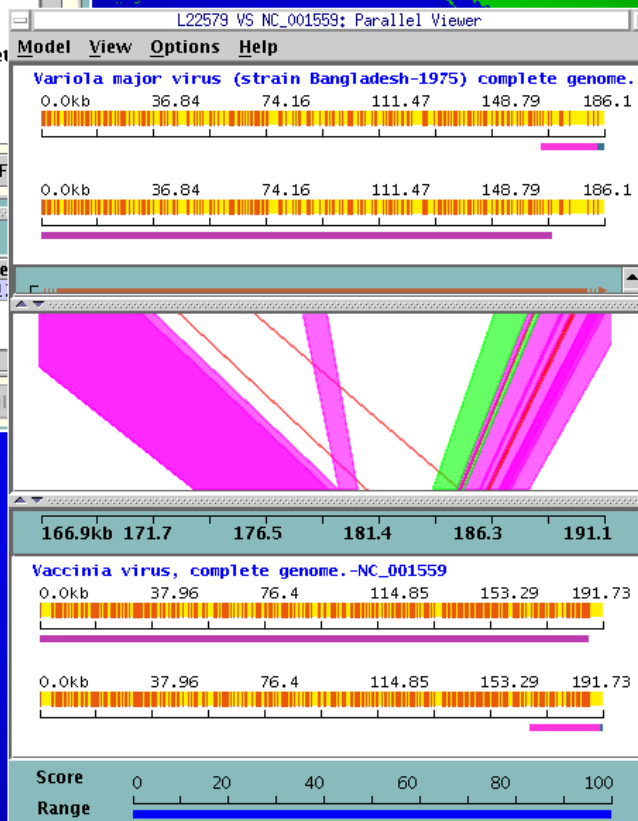
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Add Edit Use Remove

Active Tools

Tool	Status	Start	Elapse
DNA: Compare - Mum...	Completed	4/29/05 5:44 ...	00:00:1...

Stop Reuse Info Del



ToolBus

File Edit Help

Tools Views Groups

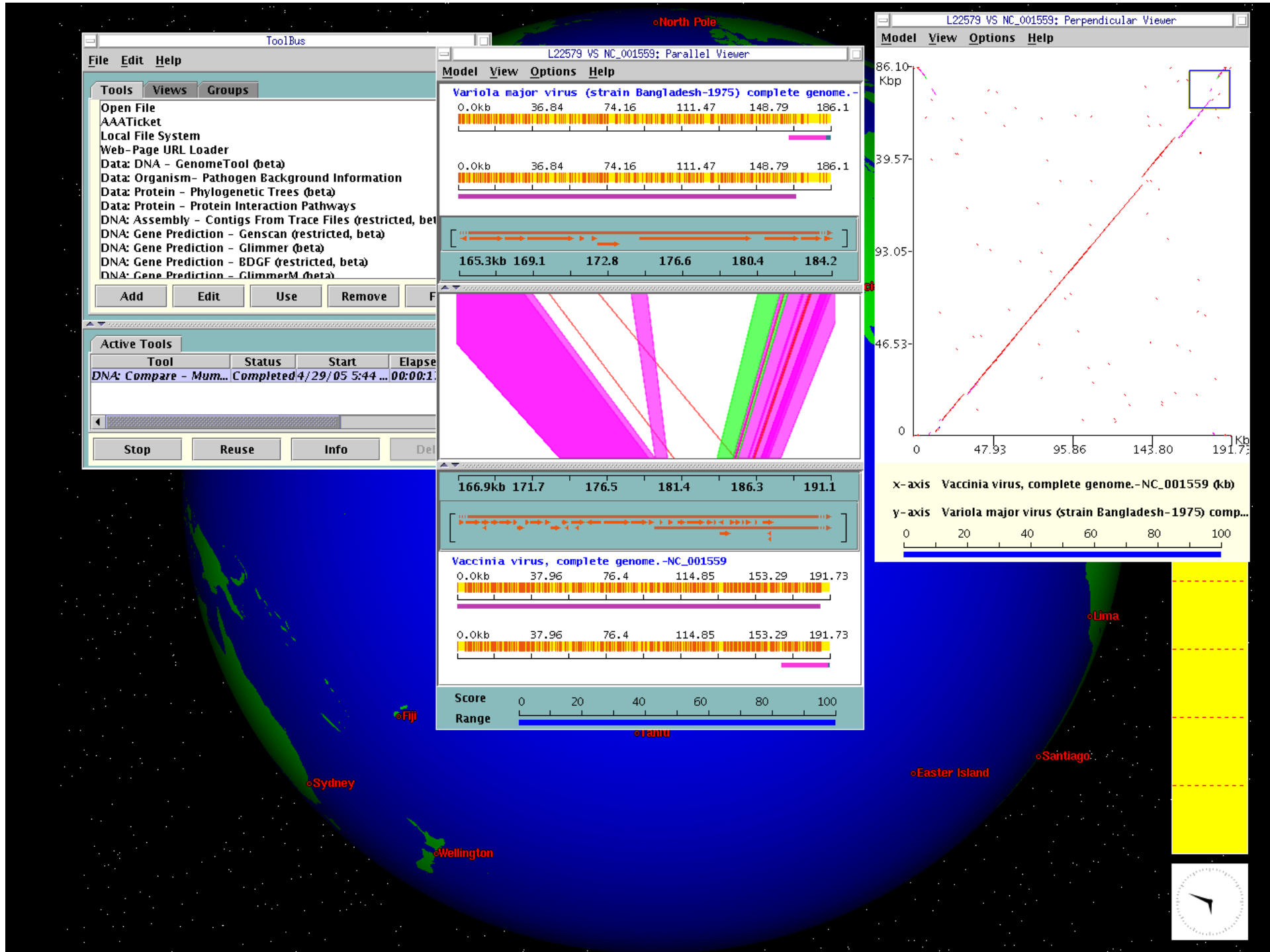
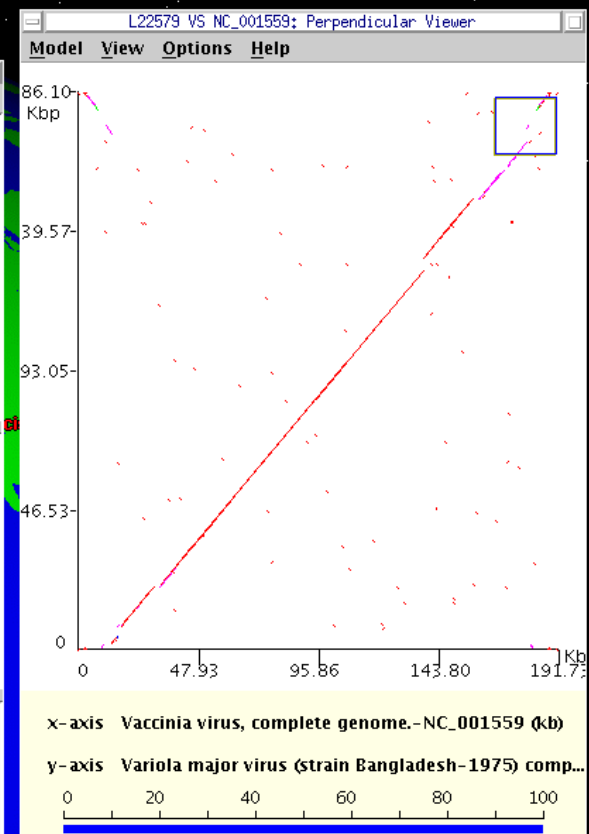
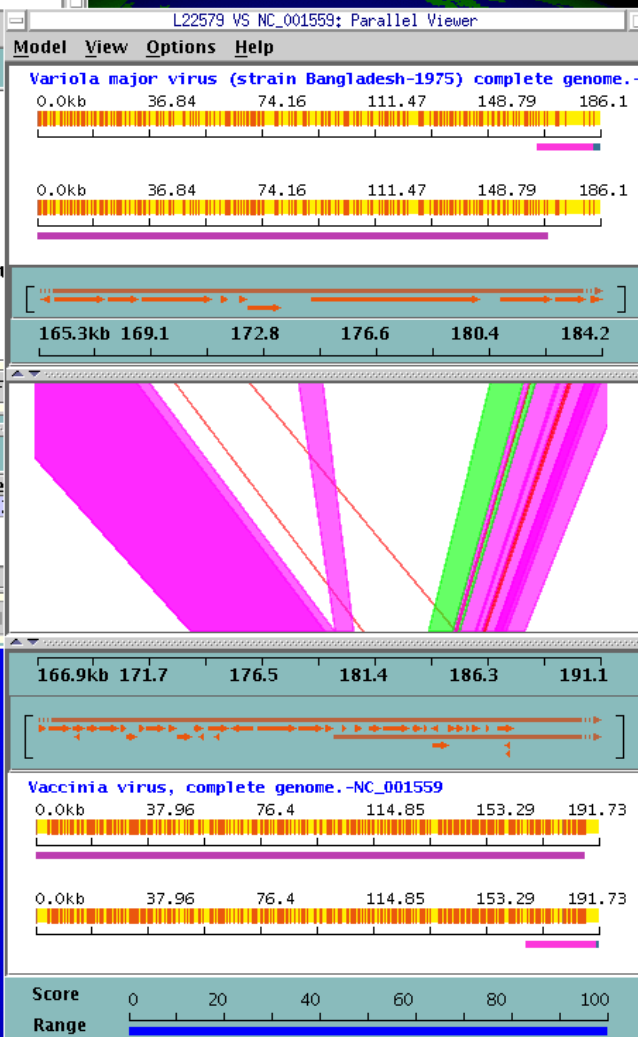
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DNA: Gene Prediction - GlimmerM (beta)

Add Edit Use Remove

Active Tools

Tool	Status	Start	Elapse
DNA: Compare - Mum...	Completed	4/29/05 5:44 ...	00:00:1...

Stop Reuse Info Del



ToolBus

File Edit Help

Tools Views Groups

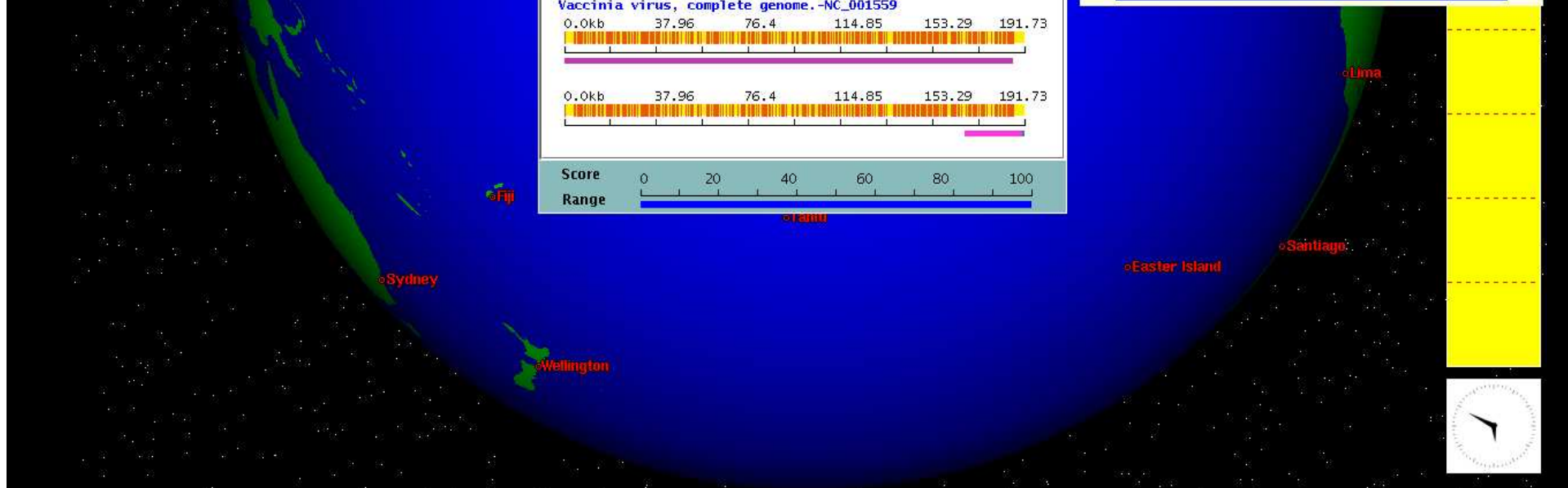
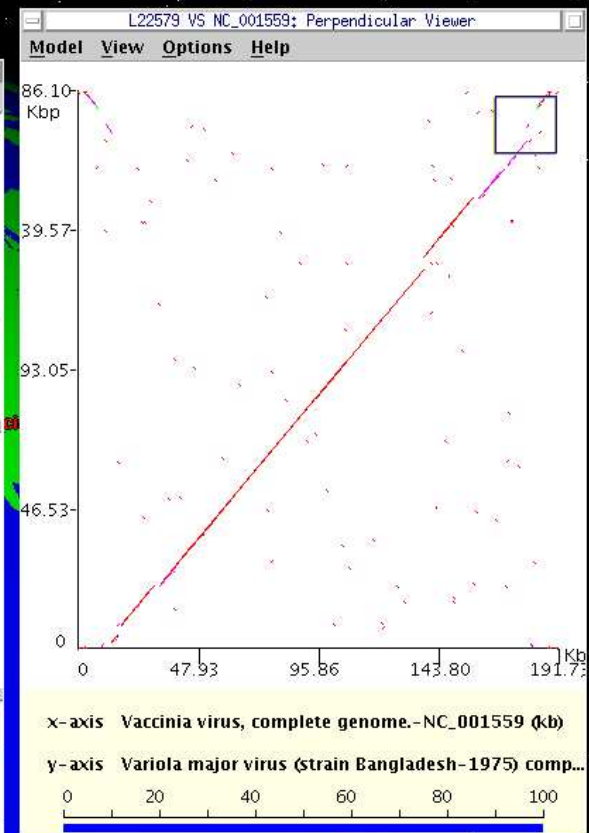
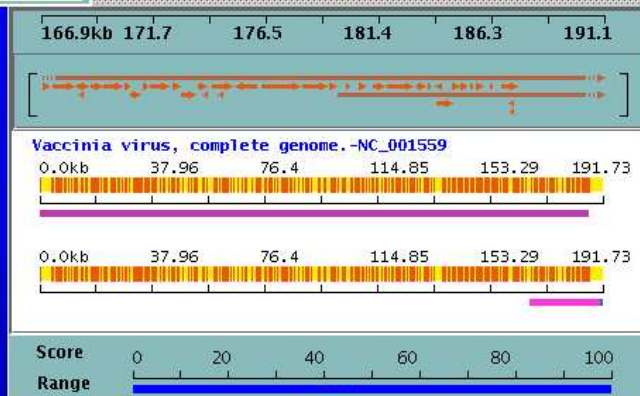
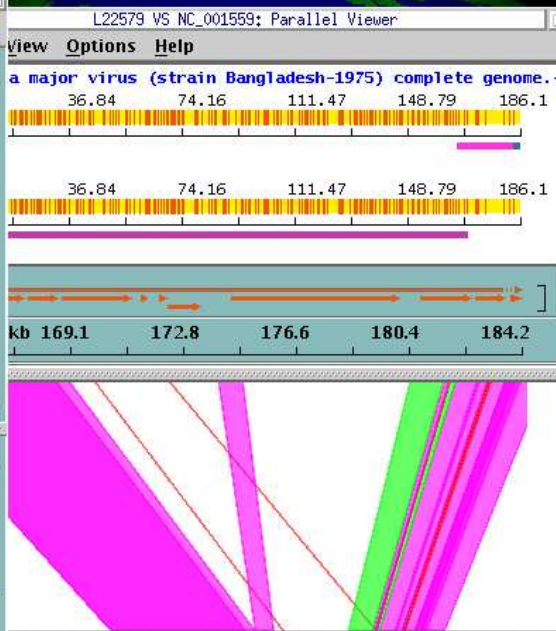
DNA: Gene Prediction - Genemark (restricted, beta)
 DNA: Gene Prediction - Orpheus (restricted, beta)
 DNA: Compare - Mummer (beta)
 Sequence: Alignment: pairwise - Stretcher (beta)
 Sequence: Alignment: pairwise - Water (beta)
 Sequence: Alignment: multiple - ClustalW (beta)
 Sequence: Search: Similar - BLAST, Cluster (beta)
 Sequence: Search: Similar - BLAST, TimeLogic (beta)
 Sequence: Search: Similar - FASTA, Cluster (beta)
 Sequence: Search: Similar - Smith-Waterman, TimeLogic (beta)
 Sequence: Search: Pattern: Protein - InterProScan (beta)
 Probe Design - PCR/Hybridization (beta)
 Probe Design - YODA (beta)

Add Edit Use Remove Find

Active Tools

Tool	Status	Start	Elapsed
DNA: Compare - Mum...	Completed	4/29/05 5:44 ...	00:00:17

Stop Reuse Info Delete



ToolBus

File Edit Help

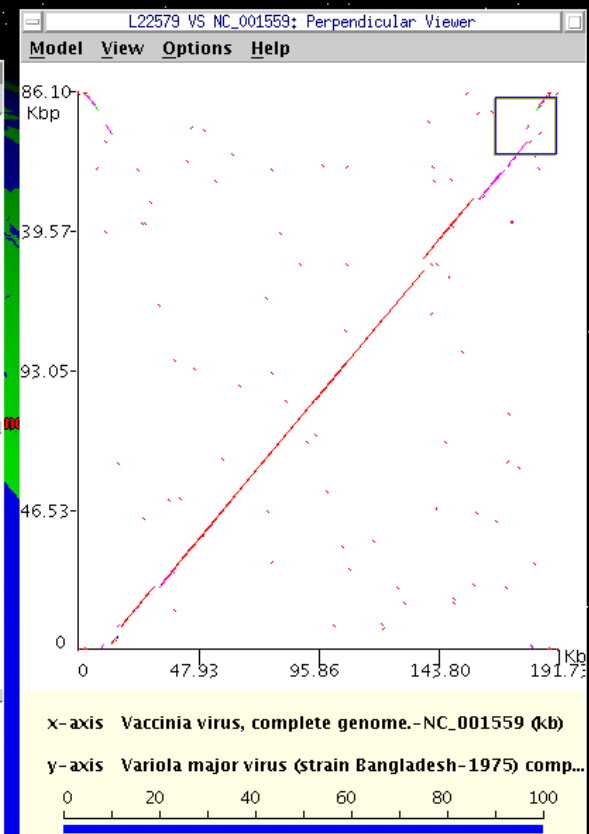
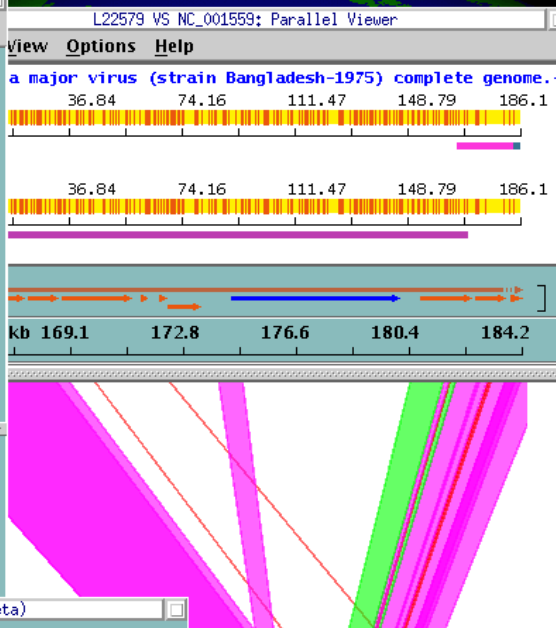
Tools Views Groups

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 Sequence: Search: Pattern: Protein - InterProScan (beta)
 Probe Design - PCR/Hybridization (beta)
 Probe Design - YODA (beta)

Add Edit Use Remove Find

Active Tools

Tool	Status	Start	Elapsed	http
Sequence: Search: Simi...	Initialize			http
DNA: Compare - Mum...	Completed	4/29/05 5:44	00:00:17	http



Use Sequence: Search: Similar - BLAST, Cluster (beta)

Sequence: Search: Similar - BLAST, Cluster (beta)

Uses VBI's Linux Beowulf cluster to run BLASTN, BLASTP and translating BLAST analyses on multiple organism databases simultaneously and combines the multiple responses into a single returned result.

blastp_Advanced translating_Blast_Advanced

blastn_Basic blastp_Basic translating_Blast_Basic blastn_Advanced

NR (NCBI) 02-14-2005 Database list

Feature: FTR_GenBank **Query sequence

TRANSLATED query - PROTEIN database [blastx] Translating program

1.0 The expectation value

Existence: 11 Extension: 1 The cost to open an existence gap and extension g

15 Dropoff value for gapped alignment

3 Word size

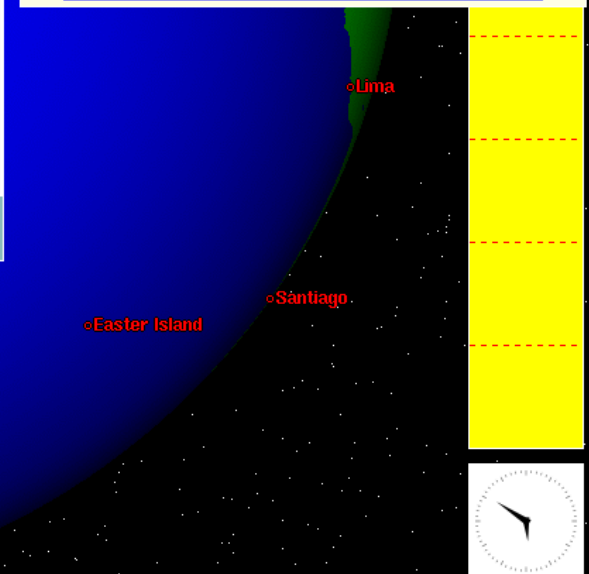
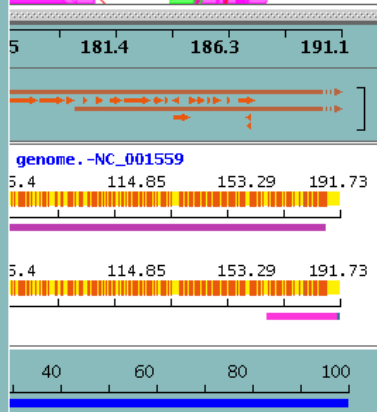
BLOSUM62 Matrix name

7 Dropoff value for ungapped extensions in bits

25 Dropoff value for final gapped alignments in bits

Both Library type (disabled if selecting NCBI database)

Run Reset About Cancel



ToolBus

File Edit Help

Tools Views Groups

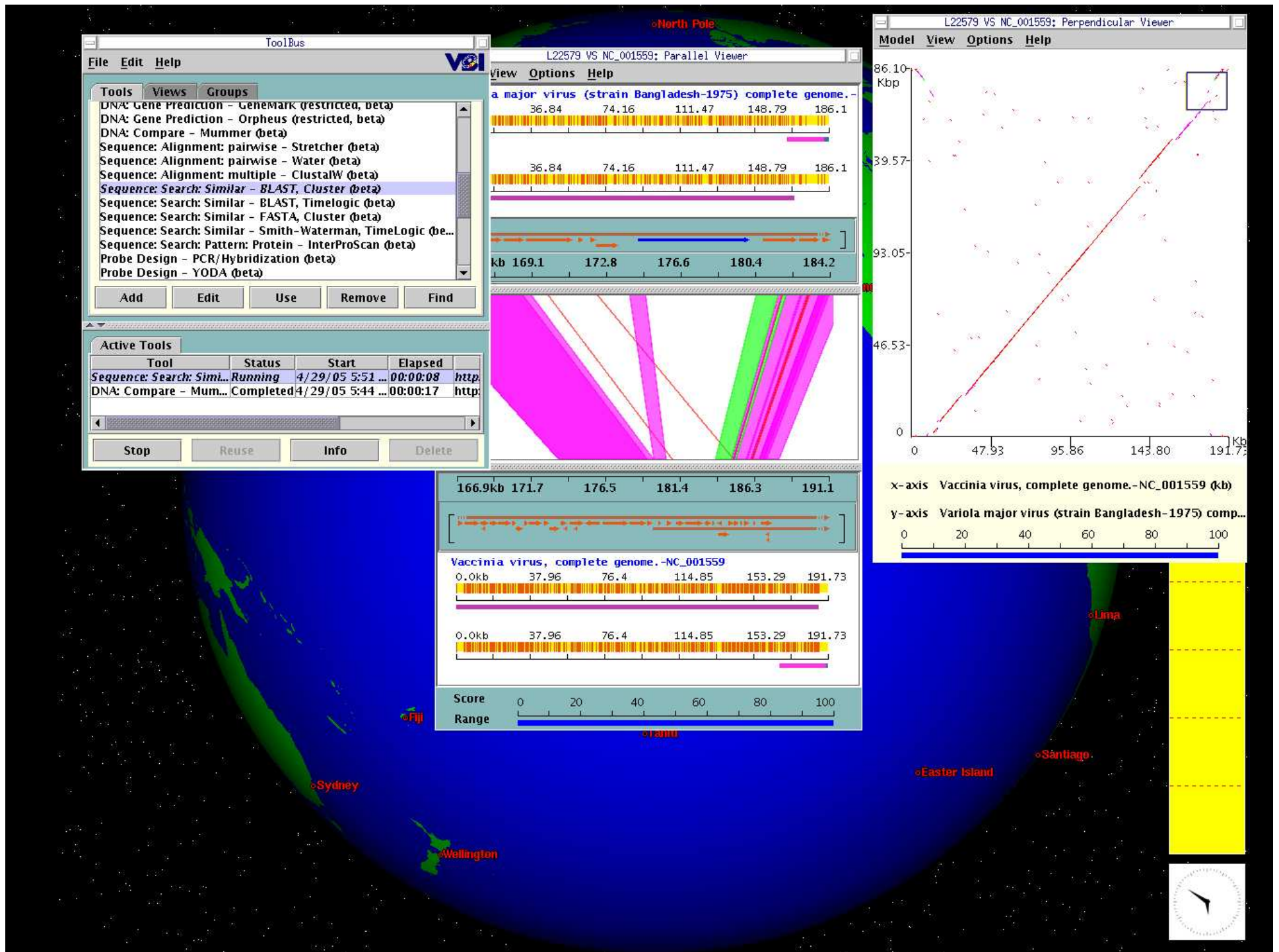
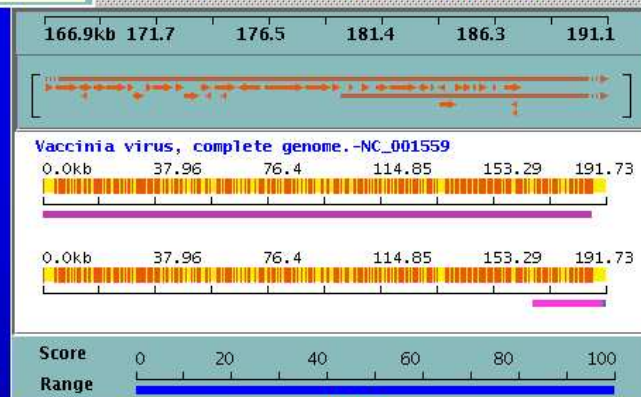
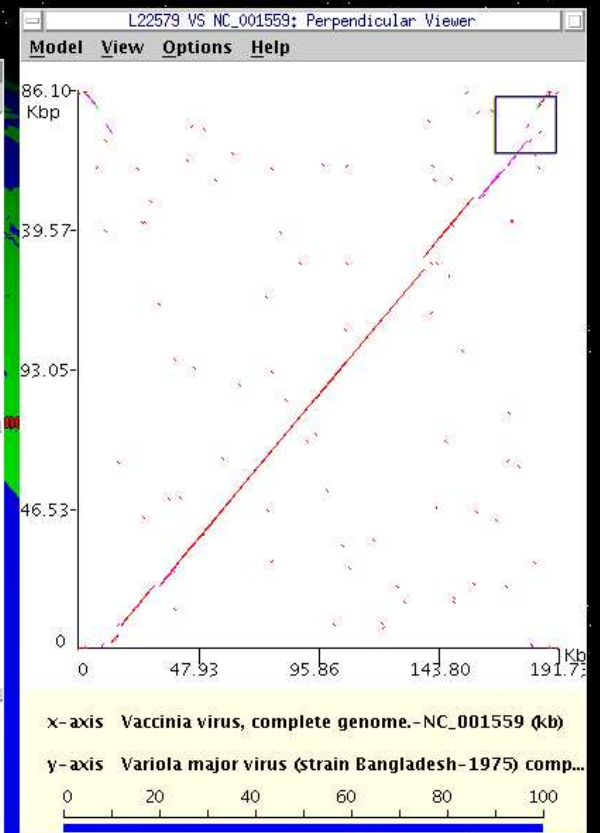
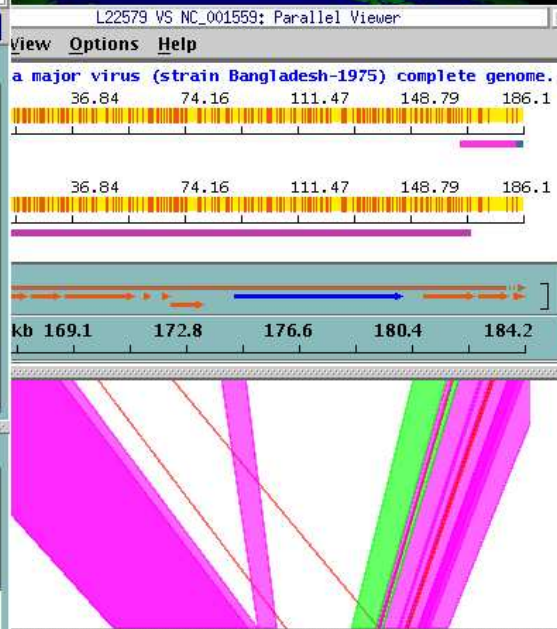
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 Sequence: Search: Similar - Smith-Waterman, TimeLogic (beta)
 Sequence: Search: Pattern: Protein - InterProScan (beta)
 Probe Design - PCR/Hybridization (beta)
 Probe Design - YODA (beta)

Add Edit Use Remove Find

Active Tools

Tool	Status	Start	Elapsed	
Sequence: Search: Simi...	Running	4/29/05 5:51 ...	00:00:08	http:
DNA: Compare - Mum...	Completed	4/29/05 5:44 ...	00:00:17	http:

Stop Reuse Info Delete



ToolBus

File Edit Help

Tools Views Groups

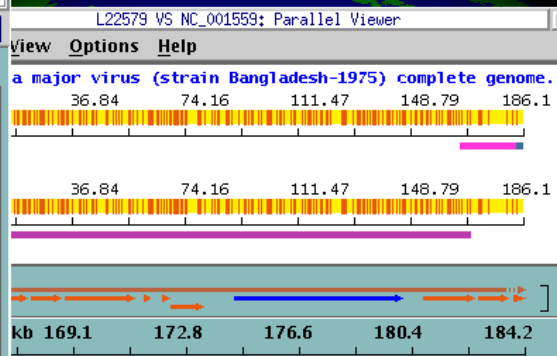
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Add Edit Use Remove Find

Active Tools

Tool	Status	Start	Elapsed	
Sequence: Search: Simi...	Completed	4/29/05 5:51 ...	00:02:26	http:
DNA: Compare - Mum...	Completed	4/29/05 5:44 ...	00:00:17	http:

Stop Reuse Info Delete



New data from Sequence: Search: Similar

Model(s) to Create

BLAST/FASTA Similarities
 Generic XML

Save Data to File

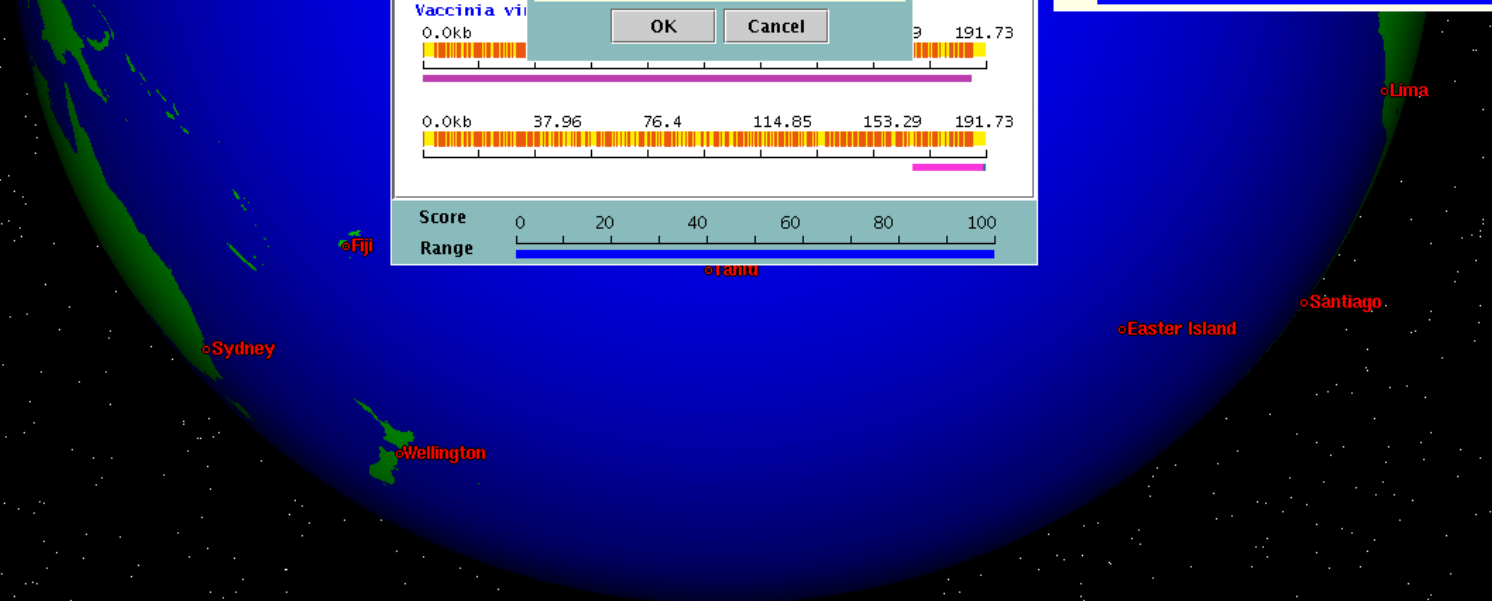
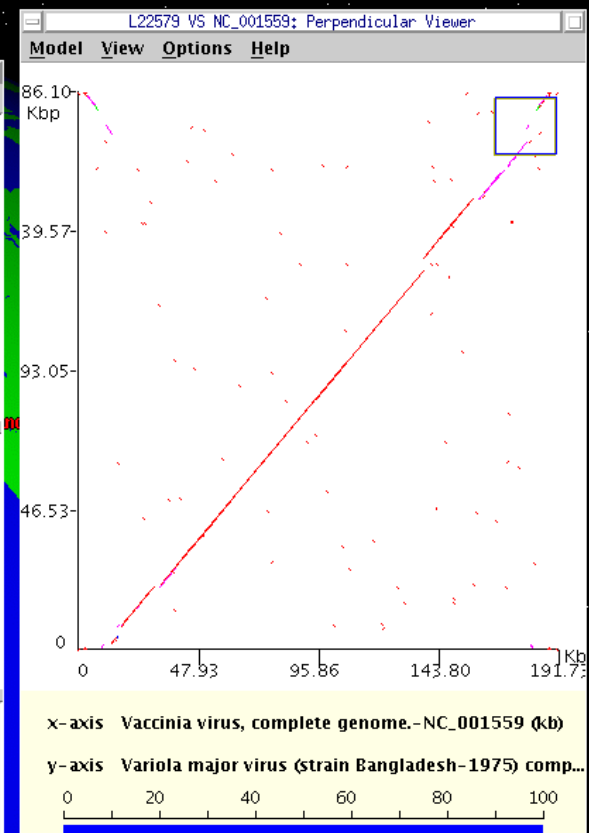
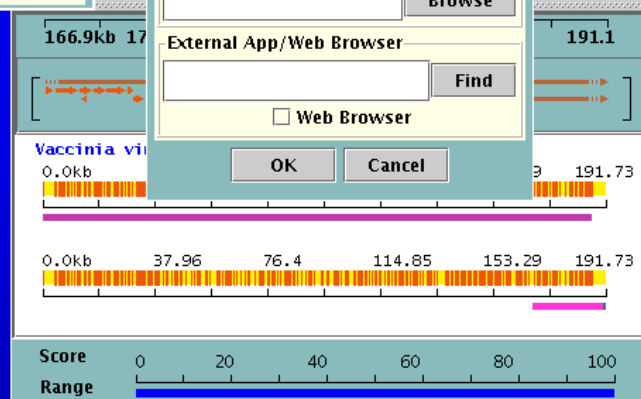
Browse

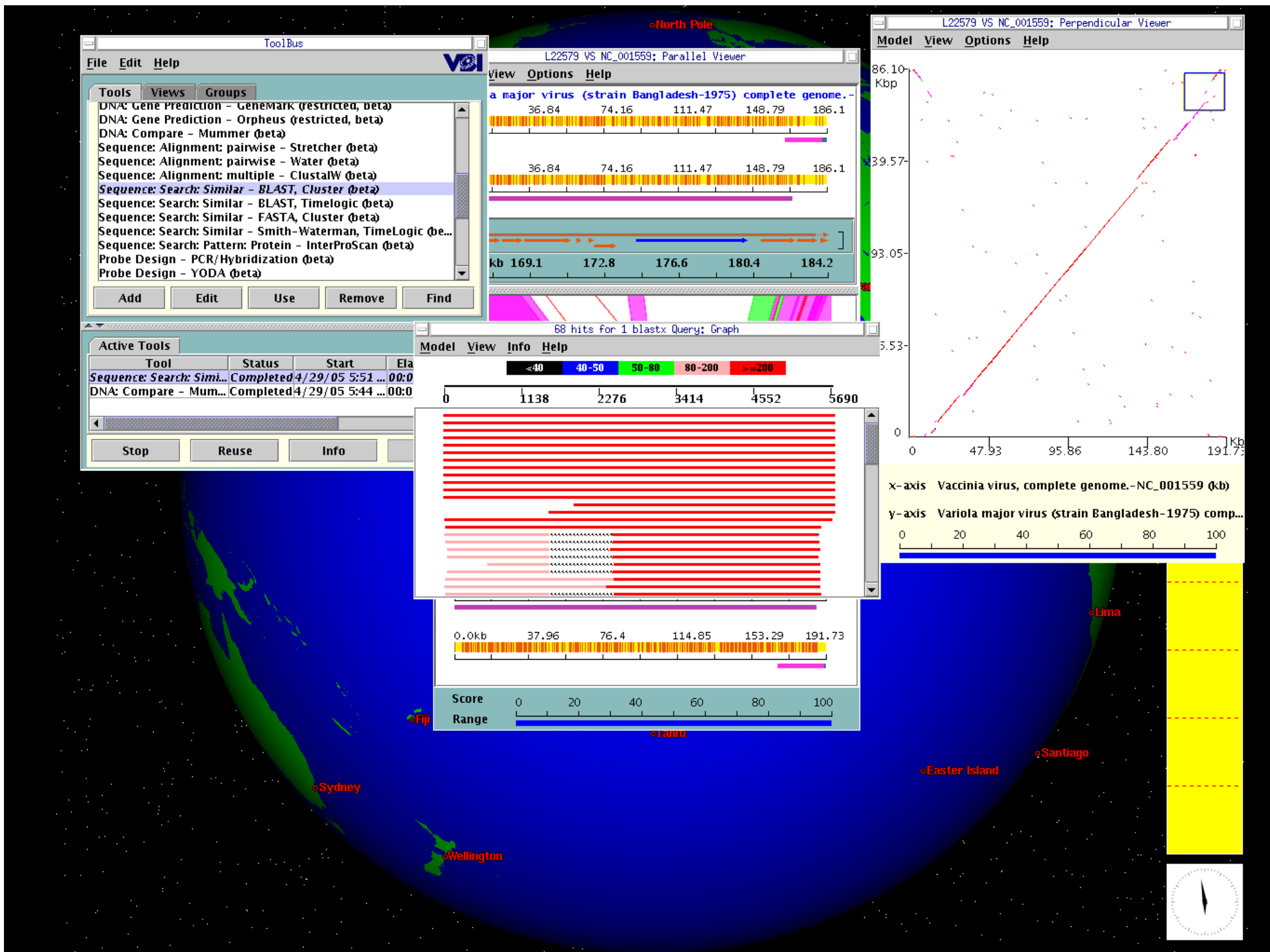
External App/Web Browser

Find

☐ Web Browser

OK Cancel





ToolBus

File Edit Help

Tools Views Groups

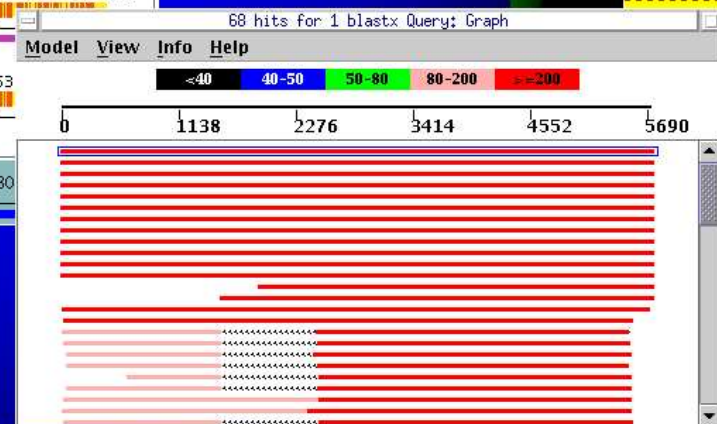
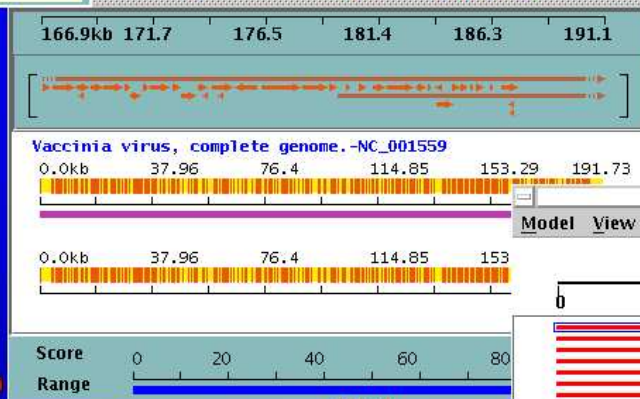
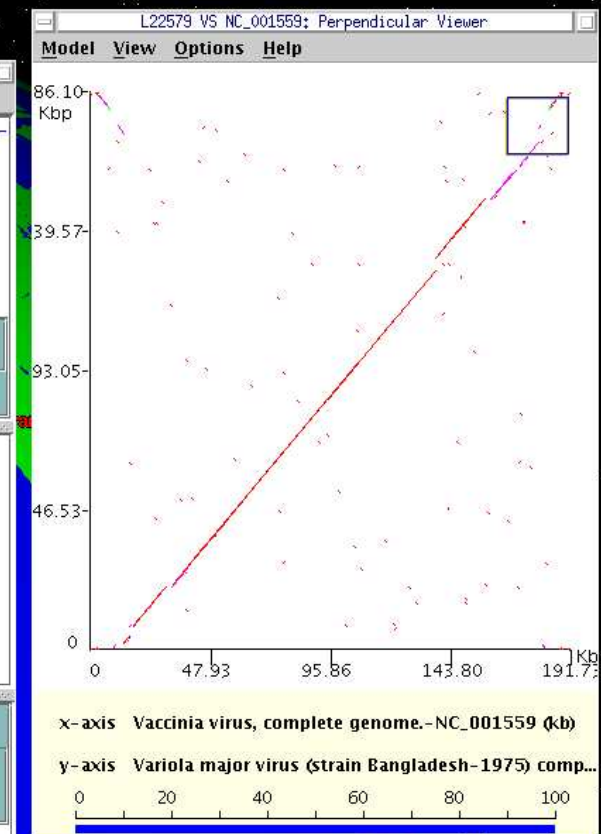
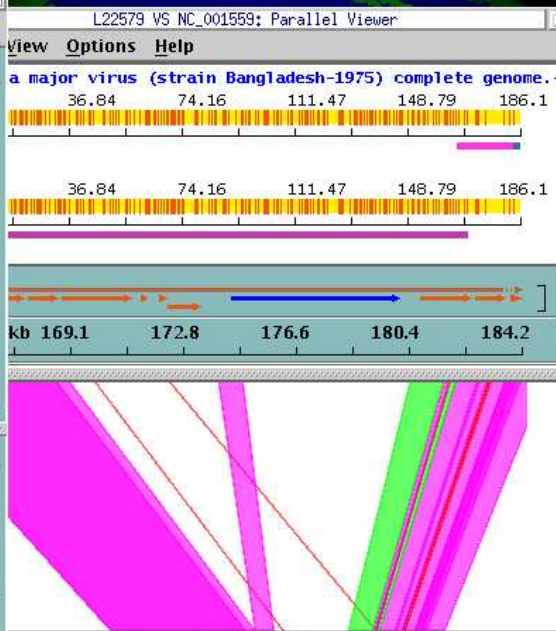
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- Sequence: Search: Similar - FASTA, Cluster (beta)
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- Sequence: Search: Pattern: Protein - InterProScan (beta)
- Probe Design - PCR/Hybridization (beta)
- Probe Design - YODA (beta)

Add Edit Use Remove Find

Active Tools

Tool	Status	Start	Elapsed	
Sequence: Search: Simi...	Completed	4/29/05 5:51 ...	00:02:26	http:
DNA: Compare - Mum...	Completed	4/29/05 5:44 ...	00:00:17	http:

Stop Reuse Info Delete



ToolBus

File Edit Help

Tools Views Groups

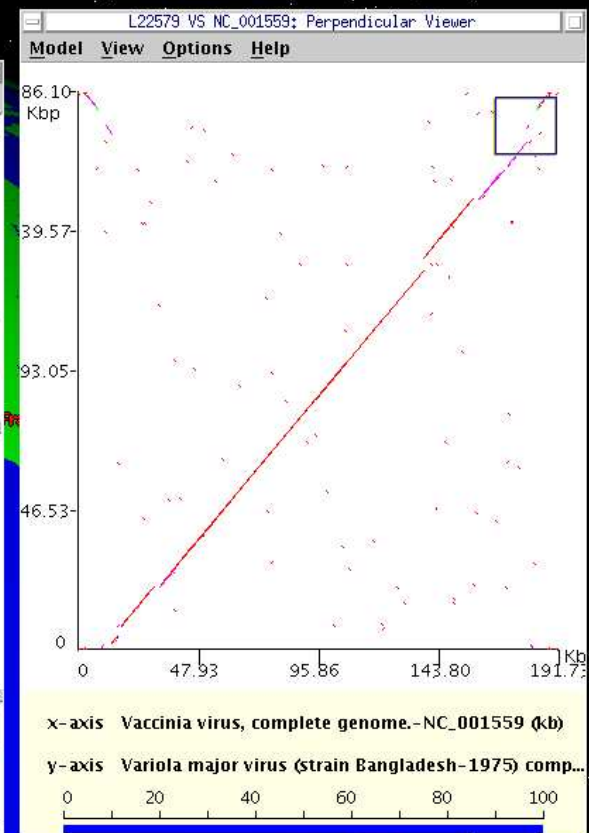
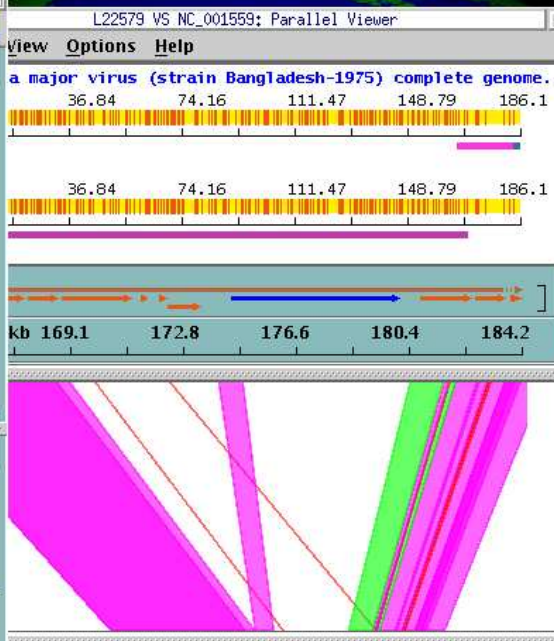
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DNA: Compare - Mum...	Completed	4/29/05 5:44	00:00:17

Stop Reuse Info Delete



gi19627715|ref|NP_042238.1|

File

>gi19627715|ref|NP_042238.1| B26R [Variola virus] >gi1457085|emb|CAA49135.1| B26R [Variola virus] >gi1745317|prf||2015436HU B26R gene
 Length = 1896

Score = 3520.3 bits (9127), Expect = 0
 Identities = 1890/1897 (99%), Positives = 1890/1897 (99%),

Query: 1 MNLQRLSLAIYLTVTCSWCYETCMRKTA LFHDNQLGHAEDNQDSVASLPYKYLQVVKRE 180
 Sbjct: 1 MNLQRLSLAIYLTVTCSWCYETCMRKTA LFHDNQLGHAEDNQDSVASLPYKYLQVVKRE 60

Web Link (protein) Web Link (nucleotide) Locate

gi17460993|pir|I28621

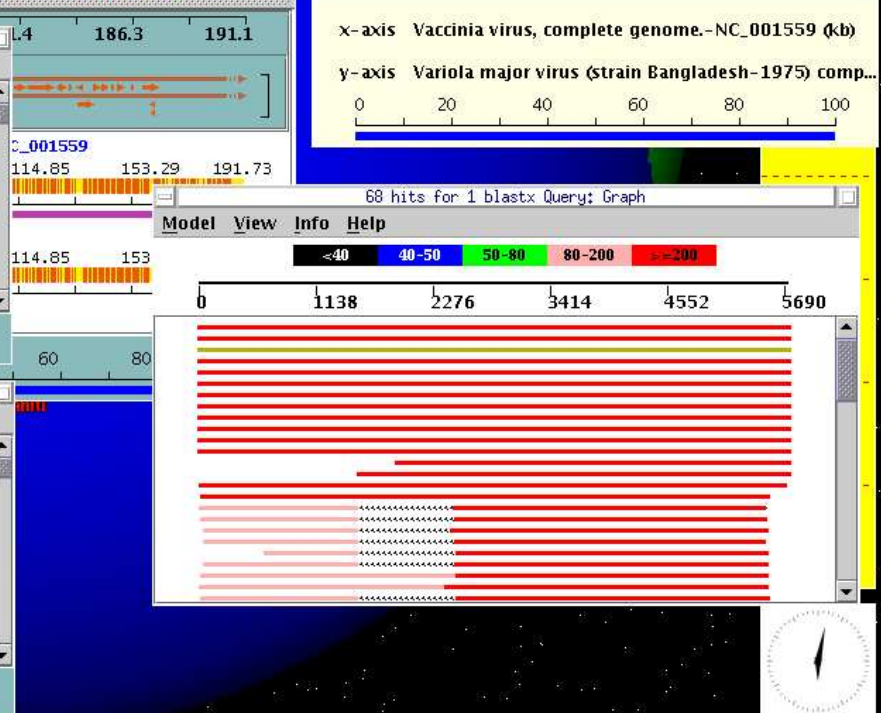
File

>gi17460993|pir|I28621 hypothetical protein B22R - variola major virus >gi1439100|gb|AAA60931.1| putative
 Length = 1897

Score = 3536.9 bits (9170), Expect = 0
 Identities = 1897/1897 (100%), Positives = 1897/1897 (100%),

Query: 1 MNLQRLSLAIYLTVTCSWCYETCMRKTA LFHDNQLGHAEDNQDSVASLPYKYLQVVKRE 180
 Sbjct: 1 MNLQRLSLAIYLTVTCSWCYETCMRKTA LFHDNQLGHAEDNQDSVASLPYKYLQVVKRE 60

Web Link (protein) Web Link (nucleotide) Locate



ToolBus

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Sequence: Alignment: pairwise - Water (beta)
Sequence: Alignment: multiple - ClustalW (beta)
Sequence: Search: Similar - BLAST, Cluster (beta)
Sequence: Search: Similar - RAST, Timelonic (beta)

NCBI Sequence Viewer v2.0 - Mozilla

File Edit View Go Bookmarks Tools Window Help

http://www.ncbi.nlm.nih.gov

NCBI

PubMed Nucleotide Protein Genome Structure PMC Taxonomy

Search Protein for

Limits Preview/Index History Clipboard Details

Display GenPept Send all to file

Range: from begin to end Features: ☐ SNP ☐ CDD ☒ MGC ☐ HPRD ☐ STS

1: [NP_042238](#). Reports B26R [Variola vir...[gi:9627715] Domains

LOCUS NP_042238 1896 aa linear VRL 20-APR-2005

DEFINITION B26R [Variola virus].

ACCESSION NP_042238

VERSION NP_042238.1 GI:9627715

DBSOURCE REFSEQ: accession [NC_001611.1](#)

KEYWORDS

SOURCE Variola virus

ORGANISM [Variola virus](#)
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae; Orthopoxvirus.

REFERENCE 1 (residues 1 to 1896)
AUTHORS Shchelkunov,S.N., Totmenin,A.V. and Sandakhchiev,L.S.
TITLE Analysis of the nucleotide sequence of 23.8 kbp from the left terminus of the genome of variola major virus strain India-1967
JOURNAL Virus Res. 40 (2), 169-183 (1996)
PUBMED [8725113](#)

REFERENCE 2
AUTHORS Shchelkunov,S.N. and Totmenin,A.V.
TITLE Two types of deletions in orthopoxvirus genomes
JOURNAL Virus Genes 9 (3), 231-245 (1995)
PUBMED [7597802](#)

REFERENCE 3 (residues 1 to 1896)
AUTHORS Shchelkunov,S.N., Blinov,V.M., Resenchuk,S.M., Totmenin,A.V., Olenina,L.V., Chirikova,G.B. and Sandakhchiev,L.S.
TITLE Analysis of the nucleotide sequence of 53 kbp from the right terminus of the genome of variola major virus strain India-1967
JOURNAL Virus Res. 34 (3), 207-236 (1994)
PUBMED [7856312](#)

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final

North Pole

L22579 VS NC_001559: Perpendicular Viewer

NCBI Sequence Viewer v2.0 - Mozilla

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Back Forward Reload Stop

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Search

Print

NCBI

PubMed Nucleotide Protein Genome Structure PMC Taxonomy

Search Protein for

Limits Preview/Index History Clipboard Details

Display GenPept Send all to file

Range: from begin to end Features: ☐ SNP ☐ CDD ☒ MGC ☐ HPRD ☐ STS

1: [T28621](#). Reports hypothetical prot...[gi:7460993] BLink, Domains, Links

LOCUS T28621 1897 aa linear VRL 21-JUL-2000

DEFINITION hypothetical protein B22R - variola major virus.

ACCESSION T28621

VERSION T28621 GI:7460993

DBSOURCE pir: locus T28621;

summary: #length 1897 #molecular-weight 213640 #checksum 3193
; PIR dates: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000

KEYWORDS

SOURCE Variola major virus

ORGANISM [Variola major virus](#)
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae; Orthopoxvirus.

REFERENCE 1 (residues 1 to 1897)
AUTHORS Massung,R.F., Esposito,J.J., Liu,L.I., Qi,J., Utterback,T.R., Knight,J.C., Aubin,L., Yuran,T.E., Parsons,J.M., Loparev,V.N. et al.
TITLE Potential virulence determinants in terminal regions of variola smallpox virus genome
JOURNAL Nature 366 (6457), 748-751 (1993)
PUBMED [8264798](#)

FEATURES

source Location/Qualifiers
1..1897
/organism="Variola major virus"
/db_xref="taxon:12870"
1..1897
product="hypothetical protein B22R"

[Protein](#)

ToolBus

File Edit Help

Tools Views Groups

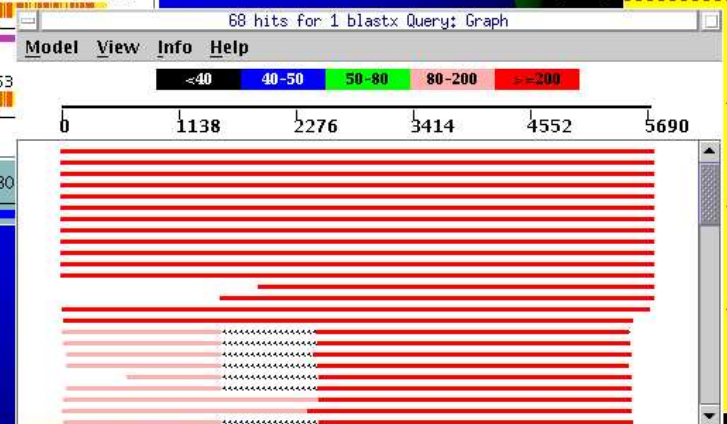
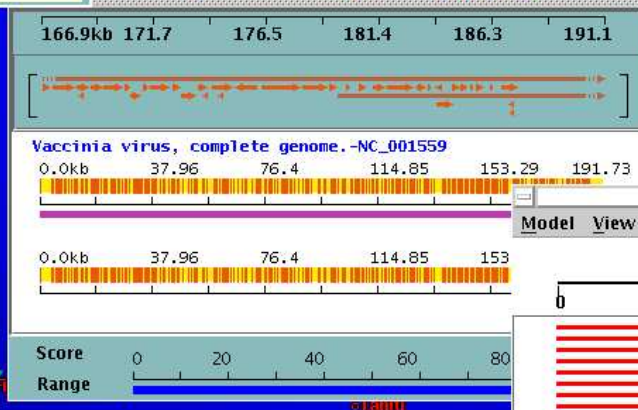
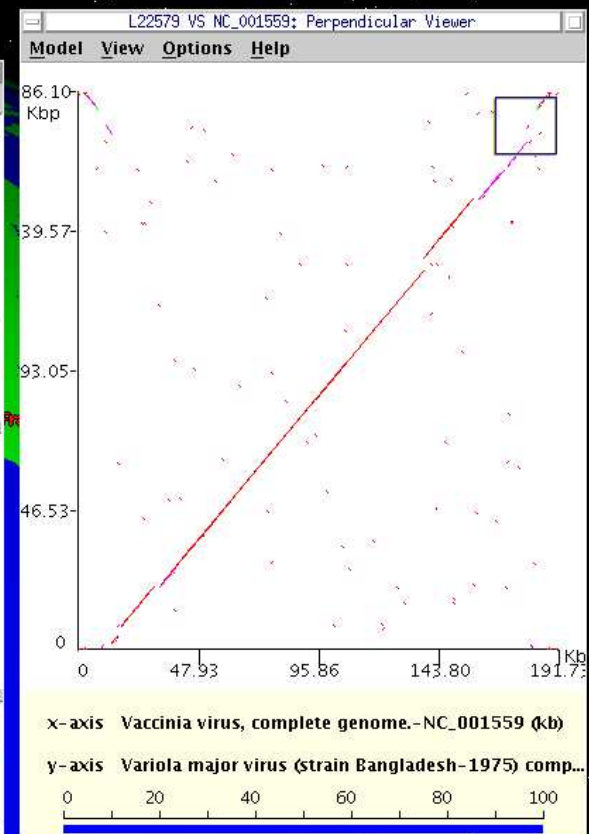
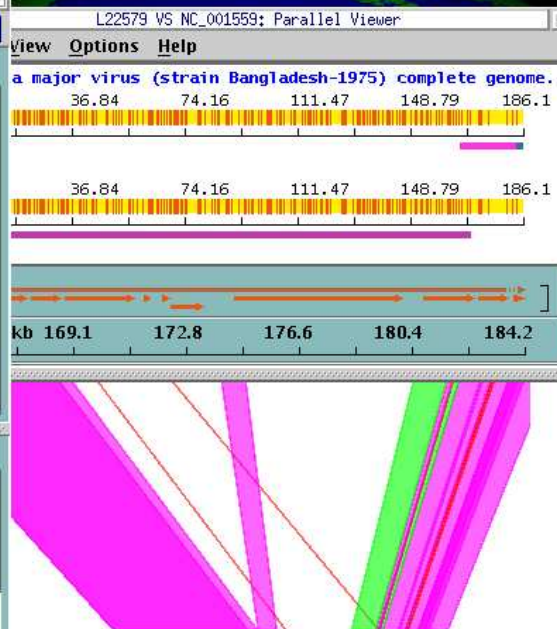
- DNA: Gene Prediction - Genemark (restricted, beta)
- DNA: Gene Prediction - Orpheus (restricted, beta)
- DNA: Compare - Mummer (beta)
- Sequence: Alignment: pairwise - Stretcher (beta)
- Sequence: Alignment: pairwise - Water (beta)
- Sequence: Alignment: multiple - ClustalW (beta)
- Sequence: Search: Similar - BLAST, Cluster (beta)
- Sequence: Search: Similar - BLAST, TimeLogic (beta)
- Sequence: Search: Similar - FASTA, Cluster (beta)
- Sequence: Search: Similar - Smith-Waterman, TimeLogic (beta)
- Sequence: Search: Pattern: Protein - InterProScan (beta)
- Probe Design - PCR/Hybridization (beta)
- Probe Design - YODA (beta)

Add Edit Use Remove Find

Active Tools

Tool	Status	Start	Elapsed
Sequence: Search: Simi...	Completed	4/29/05 5:51 ...	00:02:26
DNA: Compare - Mum...	Completed	4/29/05 5:44 ...	00:00:17

Stop Reuse Info Delete



ToolBus

File Edit Help

Tools Views Groups

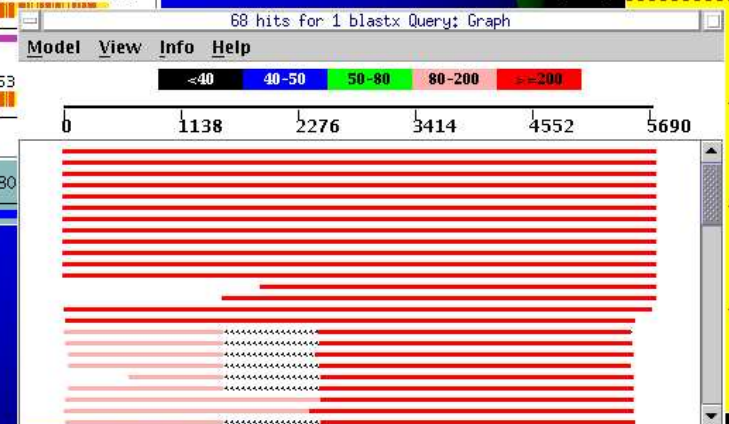
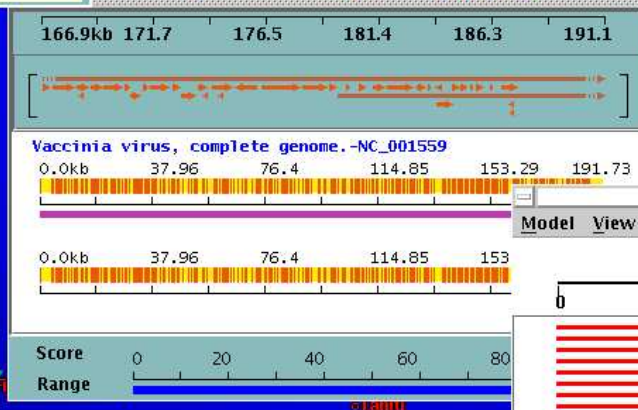
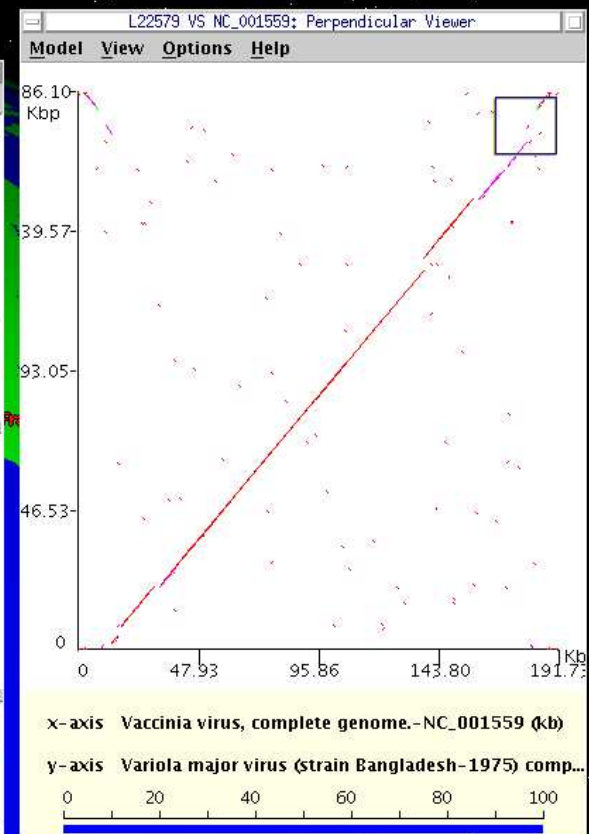
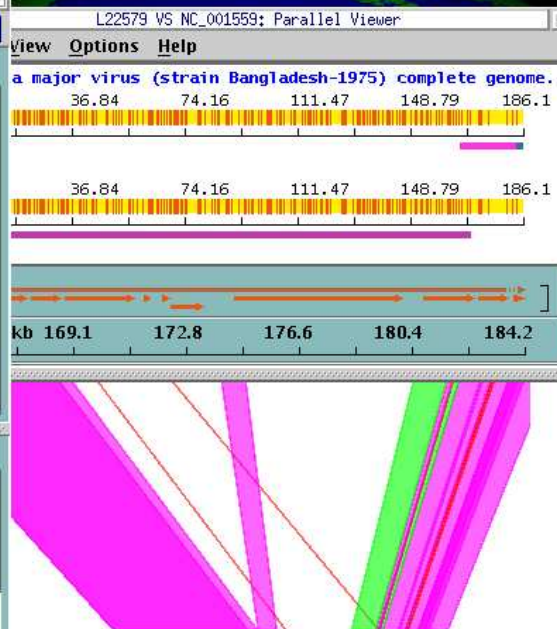
- DNA: Gene Prediction - Genemark (restricted, beta)
- DNA: Gene Prediction - Orpheus (restricted, beta)
- DNA: Compare - Mummer (beta)
- Sequence: Alignment: pairwise - Stretcher (beta)
- Sequence: Alignment: pairwise - Water (beta)
- Sequence: Alignment: multiple - ClustalW (beta)
- Sequence: Search: Similar - BLAST, Cluster (beta)
- Sequence: Search: Similar - BLAST, Timelogic (beta)
- Sequence: Search: Similar - FASTA, Cluster (beta)
- Sequence: Search: Similar - Smith-Waterman, TimeLogic (beta)
- Sequence: Search: Pattern: Protein - InterProScan (beta)
- Probe Design - PCR/Hybridization (beta)
- Probe Design - YODA (beta)

Add Edit Use Remove Find

Active Tools

Tool	Status	Start	Elapsed
Sequence: Search: Simi...	Completed	4/29/05 5:51 ...	00:02:26
DNA: Compare - Mum...	Completed	4/29/05 5:44 ...	00:00:17

Stop Reuse Info Delete



ToolBus

File Edit Help

Tools Views Groups

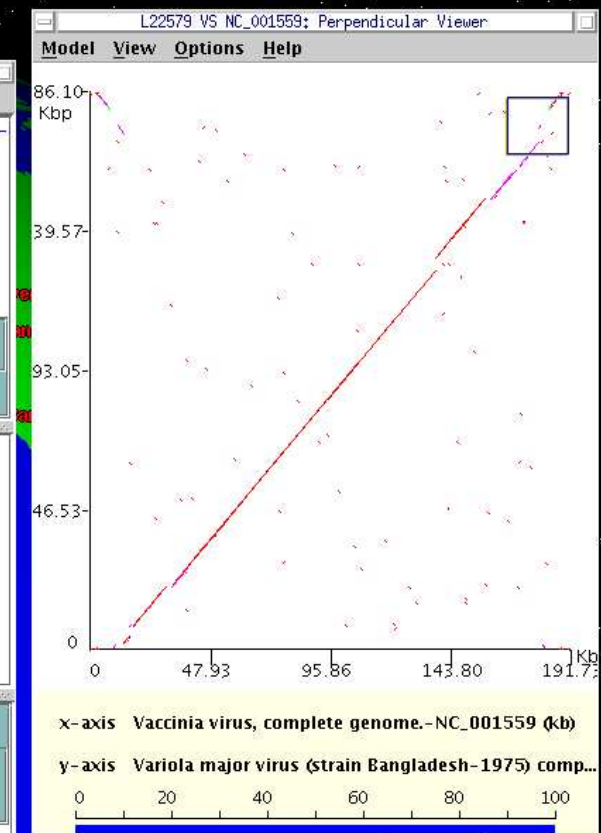
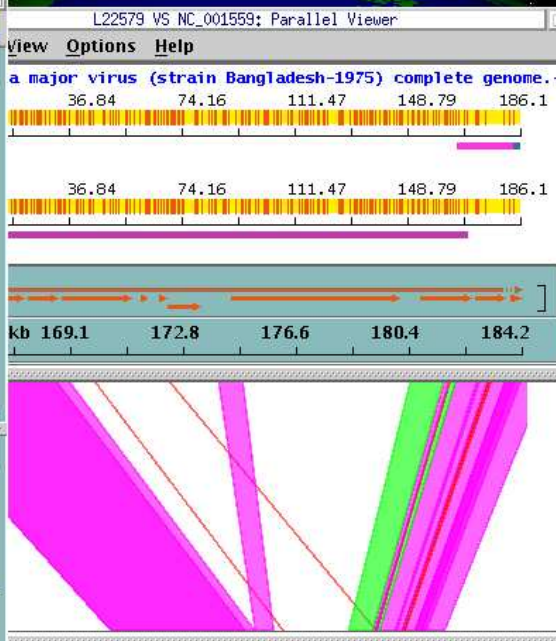
- DNA: Gene Prediction - Genemark (restricted, beta)
- DNA: Gene Prediction - Orpheus (restricted, beta)
- DNA: Compare - Mummer (beta)
- Sequence: Alignment: pairwise - Stretcher (beta)
- Sequence: Alignment: pairwise - Water (beta)
- Sequence: Alignment: multiple - ClustalW (beta)
- Sequence: Search: Similar - BLAST, Cluster (beta)
- Sequence: Search: Similar - BLAST, Timelogic (beta)
- Sequence: Search: Similar - FASTA, Cluster (beta)
- Sequence: Search: Similar - Smith-Waterman, TimeLogic (beta)
- Sequence: Search: Pattern: Protein - InterProScan (beta)
- Probe Design - PCR/Hybridization (beta)
- Probe Design - YODA (beta)

Add Edit Use Remove Find

Active Tools

Tool	Status	Start	Elapsed	http
Sequence: Alignment: ...	Initialize			http
Sequence: Search: Simi...	Completed	4/29/05 5:51	00:02:26	http
DNA: Compare - Mum...	Completed	4/29/05 5:44	00:00:17	http

Stop Reuse Info Delete



Use Sequence: Alignment: multiple - ClustalW (beta)

Sequence: Alignment: multiple - ClustalW (beta)

Multiple sequence global alignment of either DNA or protein sequences.

alignment_Basic alignment_Advanced

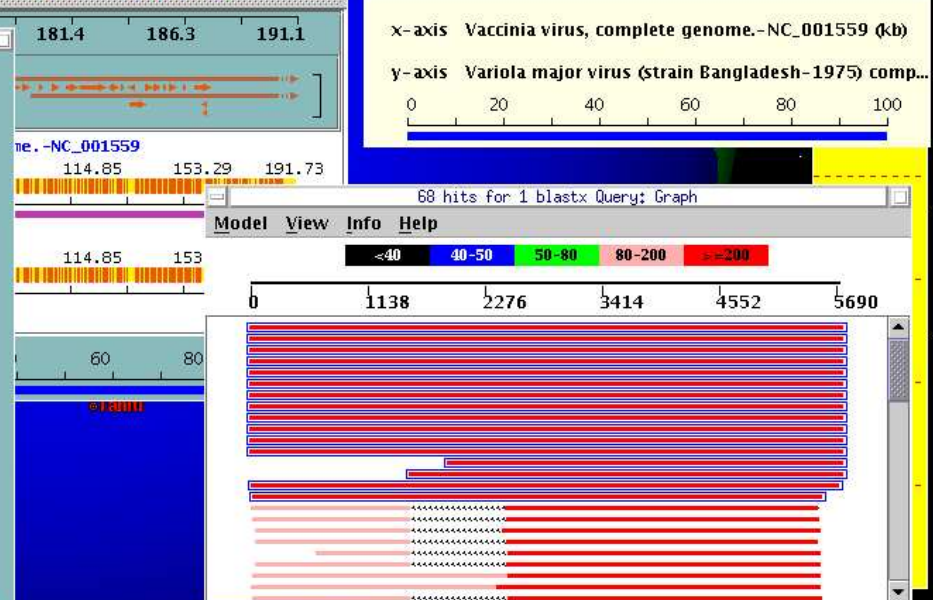
gi|41351803|gb|A/ gi|516447|emb|CA/ gi|30519573|emb/ gi|4090829

ALIGNED Output order

Nucleotide Type of sequence

Sequence Name or Id

Run Reset About Cancel



ToolBus

File Edit Help

Tools Views Groups

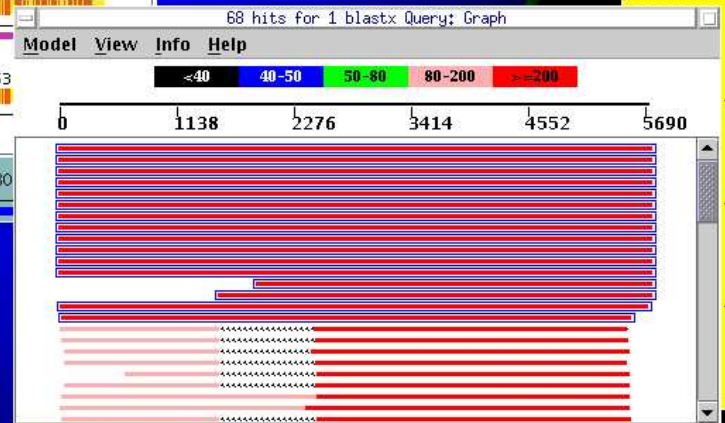
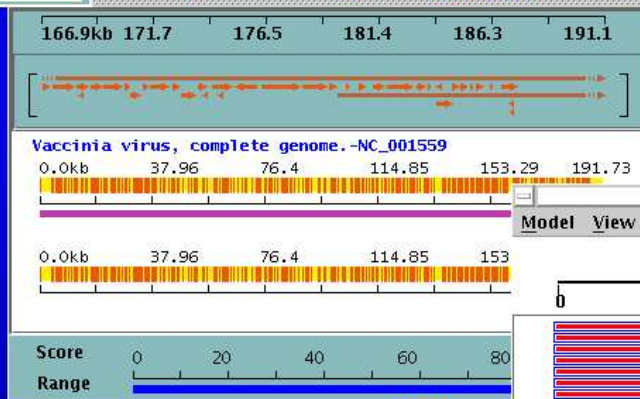
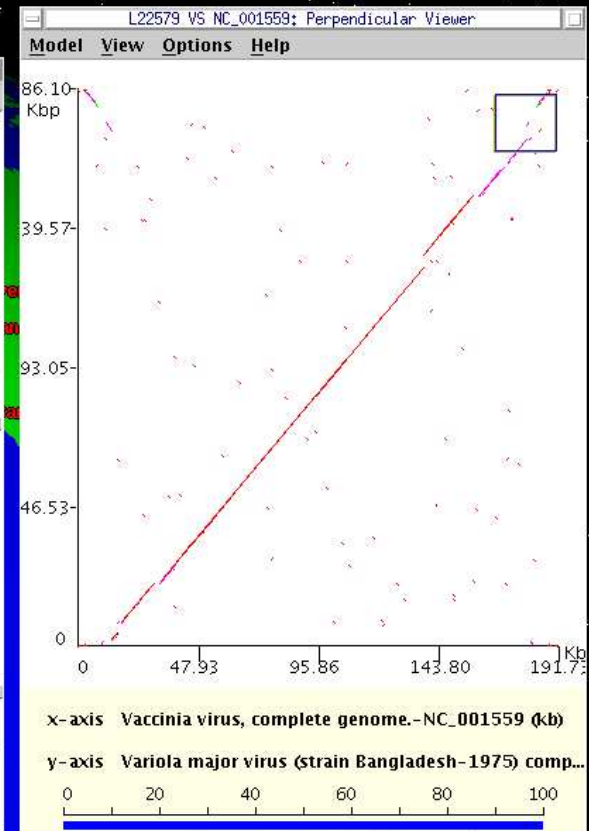
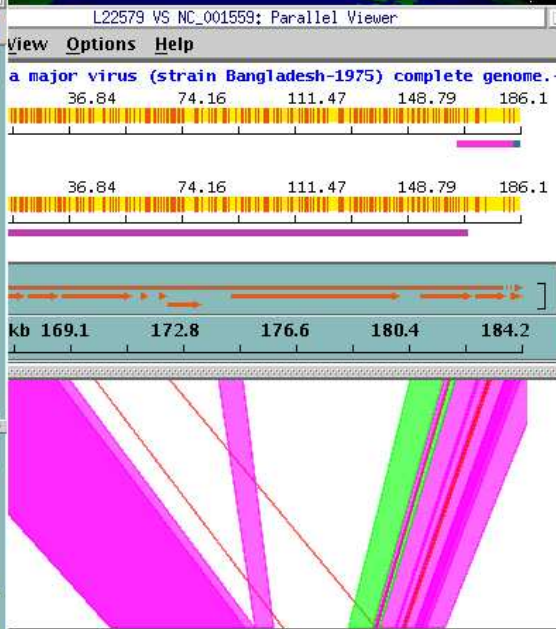
- DNA: Gene Prediction - Genemark (restricted, beta)
- DNA: Gene Prediction - Orpheus (restricted, beta)
- DNA: Compare - Mummer (beta)
- Sequence: Alignment: pairwise - Stretcher (beta)
- Sequence: Alignment: pairwise - Water (beta)
- Sequence: Alignment: multiple - ClustalW (beta)
- Sequence: Search: Similar - BLAST, Cluster (beta)
- Sequence: Search: Similar - BLAST, Timelogic (beta)
- Sequence: Search: Similar - FASTA, Cluster (beta)
- Sequence: Search: Similar - Smith-Waterman, TimeLogic (beta)
- Sequence: Search: Pattern: Protein - InterProScan (beta)
- Probe Design - PCR/Hybridization (beta)
- Probe Design - YODA (beta)

Add Edit Use Remove Find

Active Tools

Tool	Status	Start	Elapsed	http
Sequence: Alignment: ...	Running	4/29/05 6:17 ...	00:00:08	http
Sequence: Search: Simi...	Completed	4/29/05 5:51 ...	00:02:26	http
DNA: Compare - Mum...	Completed	4/29/05 5:44 ...	00:00:17	http

Stop Reuse Info Delete



ToolBus

File Edit Help

Tools Views Groups

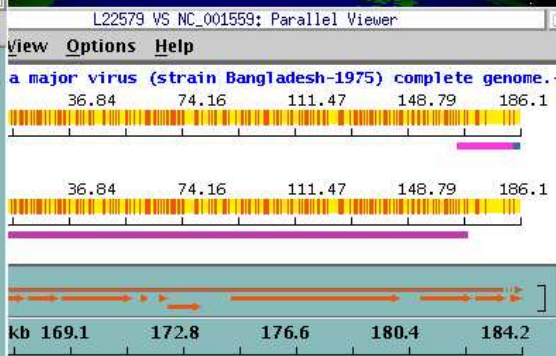
DNA: Gene Prediction - Genemark (restricted, beta)
DNA: Gene Prediction - Orpheus (restricted, beta)
DNA: Compare - Mummer (beta)
Sequence: Alignment: pairwise - Stretcher (beta)
Sequence: Alignment: pairwise - Water (beta)
Sequence: Alignment: multiple - ClustalW (beta)
Sequence: Search: Similar - BLAST, Cluster (beta)
Sequence: Search: Similar - BLAST, Timelogic (beta)
Sequence: Search: Similar - FASTA, Cluster (beta)
Sequence: Search: Similar - Smith-Waterman, TimeLogic (beta)
Sequence: Search: Pattern: Protein - InterProScan (beta)
Probe Design - PCR/Hybridization (beta)
Probe Design - YODA (beta)

Add Edit Use Remove Find

Active Tools

Tool	Status	Start	Elapsed	
Sequence: Alignment: ...	Completed	4/29/05 6:17	00:01:16	http:
Sequence: Search: Simi...	Completed	4/29/05 5:51	00:02:26	http:
DNA: Compare - Mum...	Completed	4/29/05 5:44	00:00:17	http:

Stop Reuse Info Delete



New data from Sequence: Alignment: multi

Model(s) to Create

Sequence Alignment
Generic XML

Save Data to File

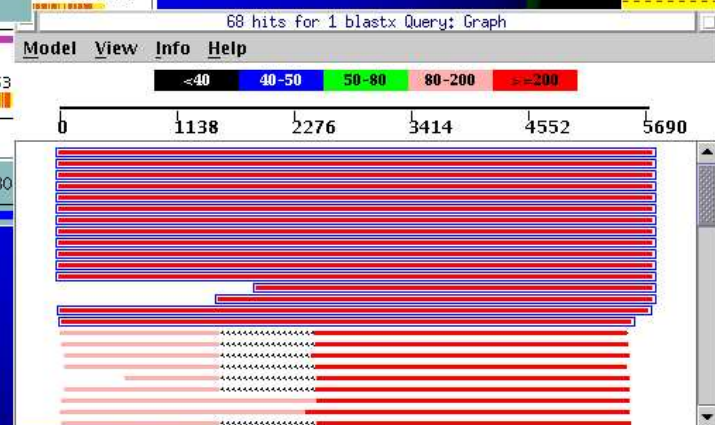
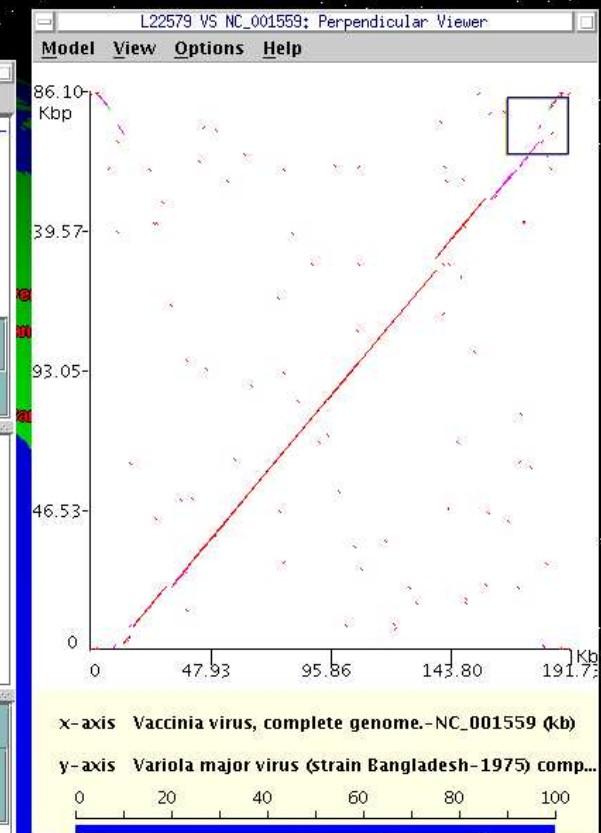
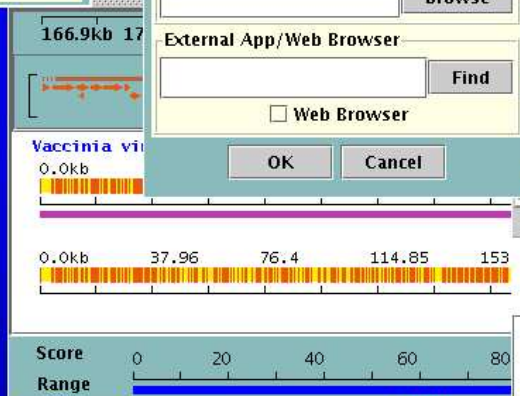
Browse

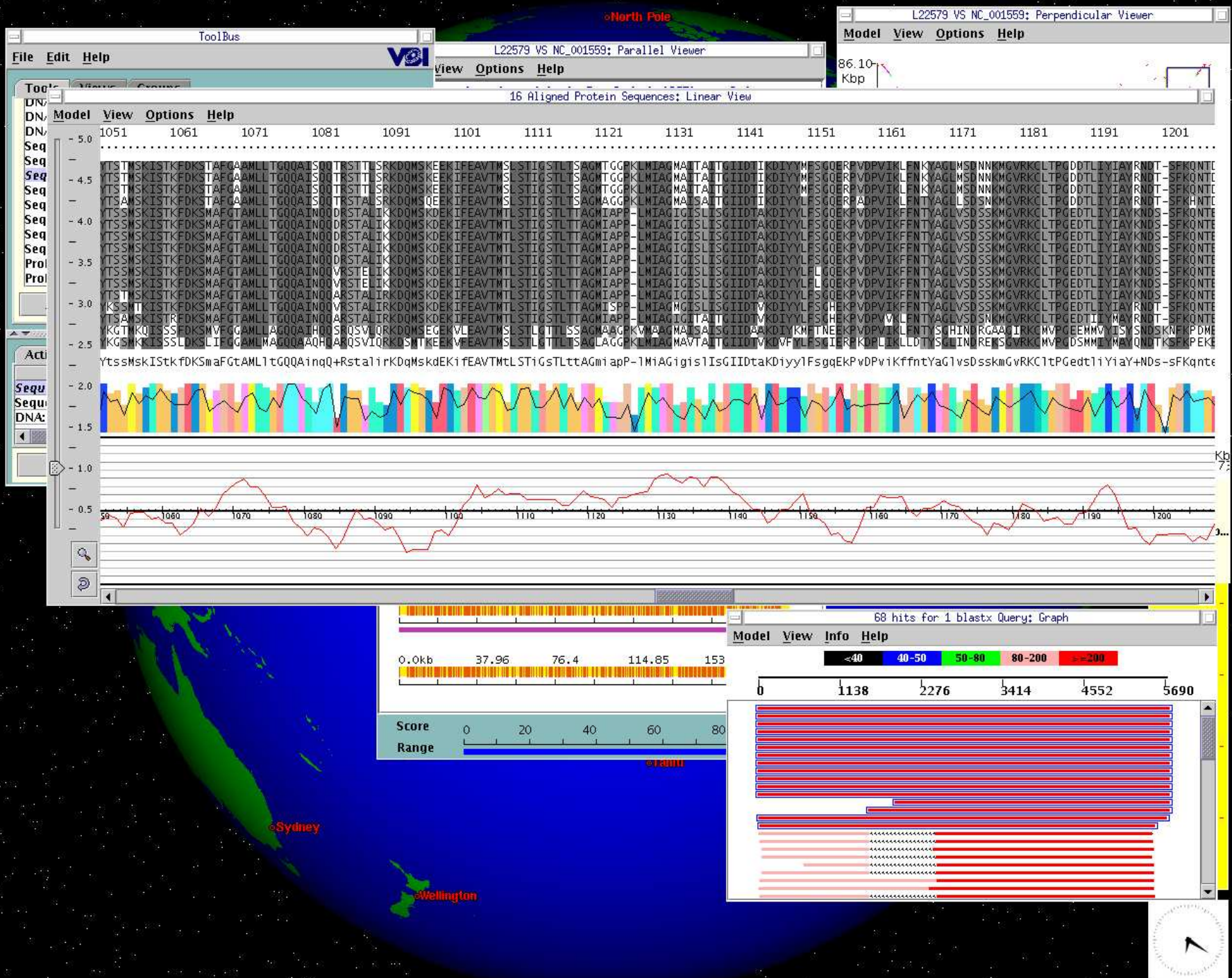
External App/Web Browser

Find

☐ Web Browser

OK Cancel





ToolBus

File Edit Help

Tools Views Groups

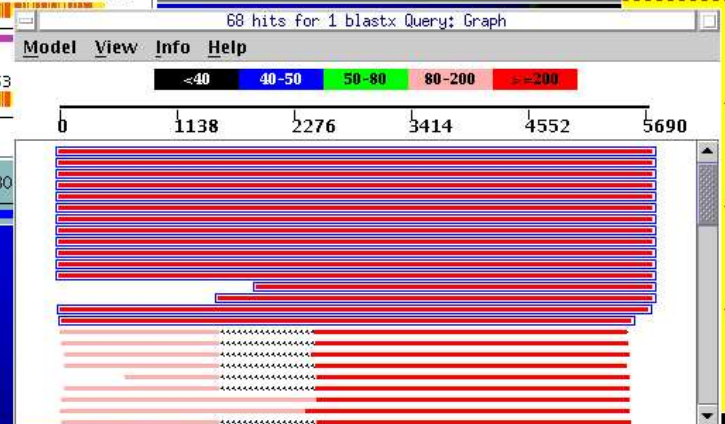
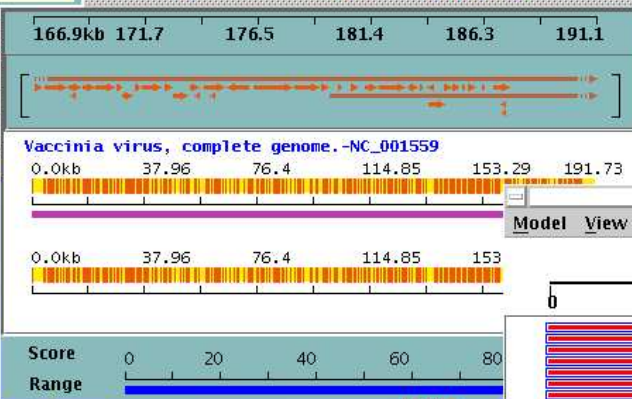
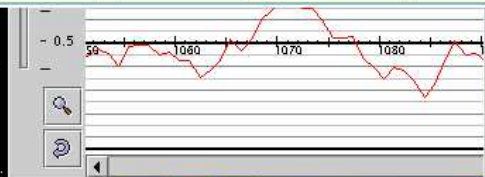
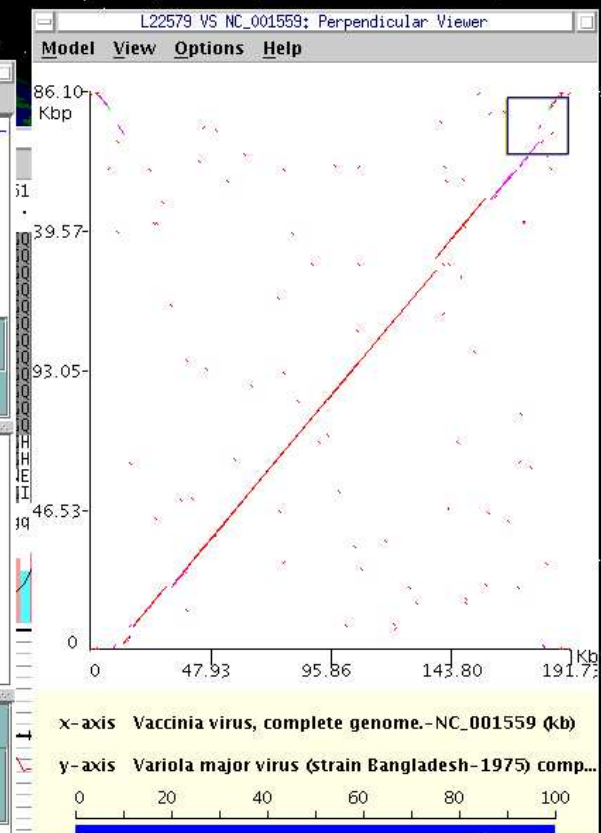
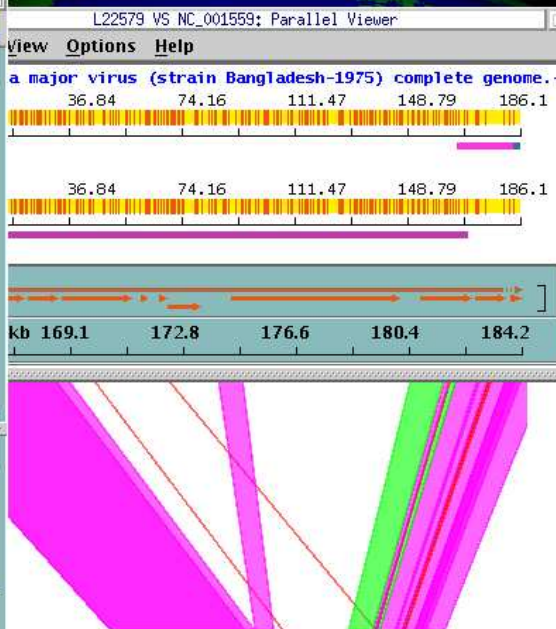
Web-Page URL Loader
Data: DNA - GenomeTool (beta)
Data: Organism - Pathogen Background Information
Data: Protein - Phylogenetic Trees (beta)
Data: Protein - Protein Interaction Pathways
DNA: Assembly - Contigs From Trace Files (restricted, beta)
DNA: Gene Prediction - Genscan (restricted, beta)
DNA: Gene Prediction - Glimmer (beta)
DNA: Gene Prediction - BDGF (restricted, beta)
DNA: Gene Prediction - GlimmerM (beta)
DNA: Gene Prediction - TigrScan (beta)
DNA: Gene Prediction - GrailEXP (restricted, beta)

Add Edit Use Remove Find

Active Tools

Tool	Status	Start	Elapsed
Sequence: Alignment: ...	Completed	4/29/05 6:17 ...	00:01:16
Sequence: Search: Simi...	Completed	4/29/05 5:51 ...	00:02:26
DNA: Compare - Mum...	Completed	4/29/05 5:44 ...	00:00:17

Stop Reuse Info Delete



ToolBus
File Edit Help

Tools Views Groups

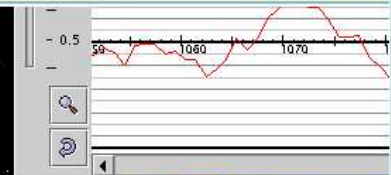
Web-Page URL Loader
Data: DNA - GenomeTool (beta)
Data: Organism - Pathogen Background Information
Data: Protein - Phylogenetic Trees (beta)
Data: Protein - Protein Interaction Pathways
DNA: Assembly - Contigs From Trace Files (restricted, beta)
DNA: Gene Prediction - Genscan (restricted, beta)
DNA: Gene Prediction - Glimmer (beta)
DNA: Gene Prediction - BDGF (restricted, beta)
DNA: Gene Prediction - GlimmerM (beta)
DNA: Gene Prediction - TigrScan (beta)
DNA: Gene Prediction - GrailEXP (restricted, beta)

Add Edit Use Remove

Active Tools

Tool	Status	Start
Data: Protein - Phylog...	Initialize	
Sequence: Alignment: ...	Completed	4/29/05 6:1
Sequence: Search: Simi...	Completed	4/29/05 5:5

Stop Reuse Info



Menu Database Help

Database "prokaryote2" - Query Options

Species/Strains Descriptions About Database

List of 184 species/strains:

Acinetobacter sp. ADP1
Aeropyrum pernix K1
Agrobacterium tumefaciens str. C58
Aquifex aeolicus VF5
Archaeoglobus fulgidus DSM 4304
Bacillus anthracis str. 'Ames Ancestor'
Bacillus anthracis str. A2012
Bacillus anthracis str. Ames
Bacillus anthracis str. ...

Selected Species/strains

Submit Query

Clear Query

Update Jobs

Alignment Based Tree Information

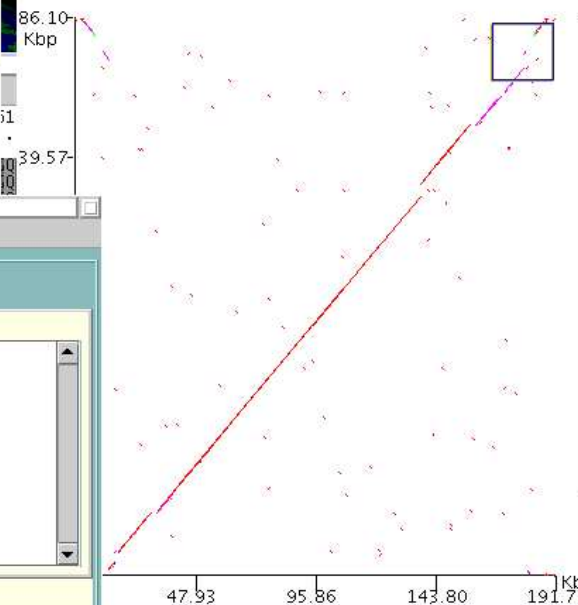
Retrieve Tree(s)

Remove

Close

L22579 VS NC_001559: Perpendicular Viewer

Model View Options Help



ToolBus

File Edit Help

Tools Views Groups

Web-Page URL Loader
Data: DNA - GenomeTool (beta)
Data: Organism - Pathogen Background Information
Data: Protein - Phylogenetic Trees (beta)
Data: Protein - Protein Interaction Pathways
DNA: Assembly - Contigs From Trace Files (restricted, beta)
DNA: Gene Prediction - Genscan (restricted, beta)
DNA: Gene Prediction - Glimmer (beta)
DNA: Gene Prediction - BDGF (restricted, beta)
DNA: Gene Prediction - GlimmerM (beta)
DNA: Gene Prediction - TigrScan (beta)
DNA: Gene Prediction - GrailEXP (restricted, beta)

Add Edit Use Remove

Active Tools

Tool	Status	Start
Data: Protein - Phylog...	Initialize	
Sequence: Alignment: ...	Completed	4/29/05 6:1
Sequence: Search: Simi...	Completed	4/29/05 5:5

Stop Reuse Info

Menu Database Help

Database "viral2" - Query Options

Species/Strains Descriptions About Database

List of 4164 genes/Annotations

Selected genes/annotations

B22R-LIKE PROTEIN

Description key words: b22r Find

Submit Query Clear Query Update Jobs

Alignment Based Tree Information

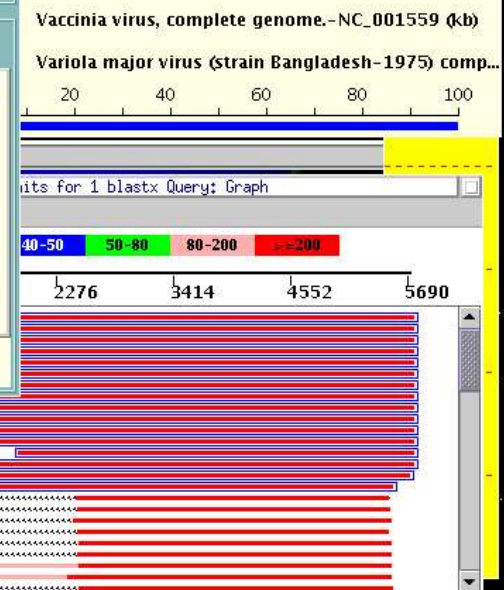
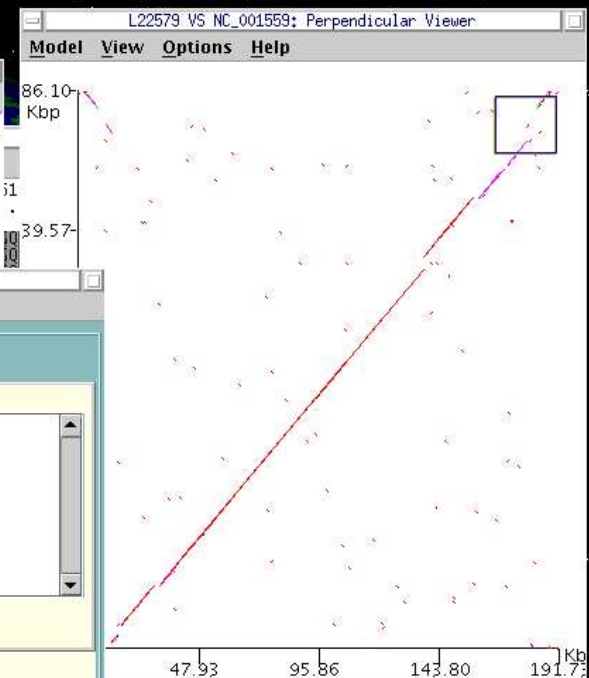
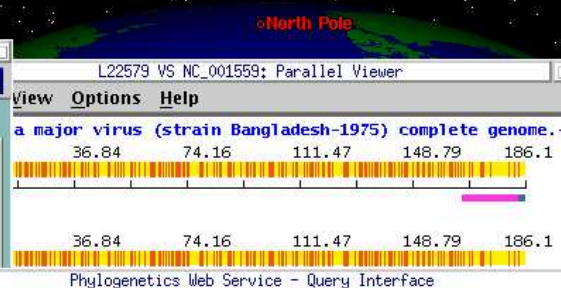
Query 1

2 protein homology groups are shown for this query.

Homolo...	Taxa	Tips	Trees	Annotation	Select
185	15	25	2	B21R	<input type="checkbox"/>
191	7	7	1	B21R	<input type="checkbox"/>

☒ Include MSA Information View Query Information

Retrieve Tree(s) Remove Close



ToolBus

File Edit Help

Tools Views Groups

Web-Page URL Loader
 Data: DNA - GenomeTool (beta)
 Data: Organism - Pathogen Background Information
 Data: Protein - Phylogenetic Trees (beta)
 Data: Protein - Protein Interaction Pathways
 DNA: Assembly - Contigs From Trace Files (restricted, beta)
 DNA: Gene Prediction - Genscan (restricted, beta)
 DNA: Gene Prediction - Glimmer (beta)
 DNA: Gene Prediction - BDGF (restricted, beta)
 DNA: Gene Prediction - GlimmerM (beta)
 DNA: Gene Prediction - TigrScan (beta)
 DNA: Gene Prediction - GrailEXP (restricted, beta)

Add Edit Use Remove

Active Tools

Tool	Status	Start
Data: Protein - Phylog...	Initialize	
Sequence: Alignment: ...	Completed	4/29/05 6:1
Sequence: Search: Simi...	Completed	4/29/05 5:5

Stop Reuse Info

Menu Database Help

Database "viral2" - Query Options

Species/Strains Descriptions About Database

List of 4164 genes/Annotations Selected genes/annotations

B19R
 B1R
 B20R
 B21R
 B22R-LIKE PROTEIN
 B25R
 B26R

Description key words: b26r Find

Submit Query Clear Query Update Jobs

Alignment Based Tree Information

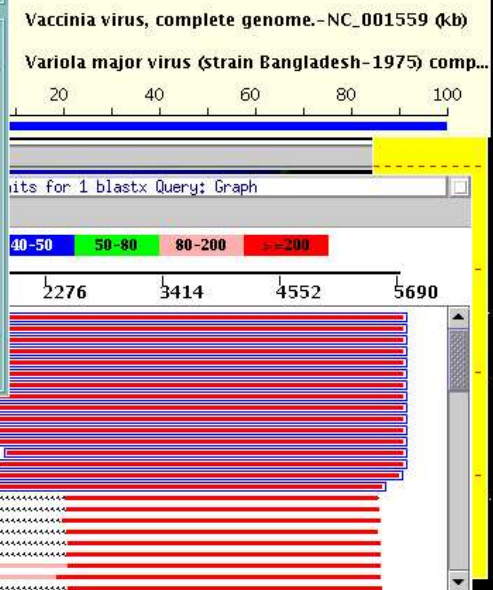
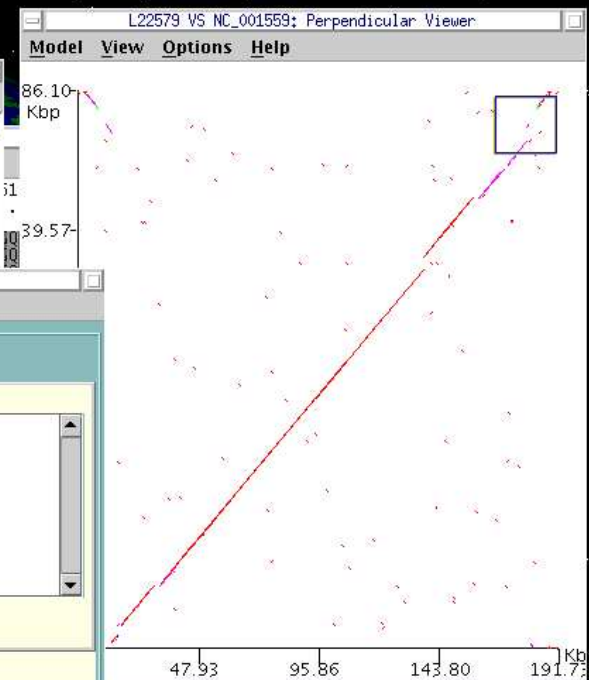
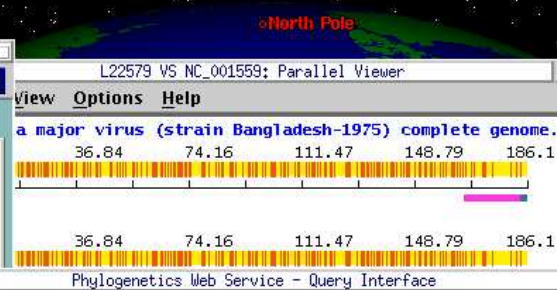
Query 1 Query 2

2 protein homology groups are shown for this query.

Homolo...	Taxa	Tips	Trees	Annotation	Select
185	15	25	2	B21R	<input type="checkbox"/>
191	7	7	1	B21R	<input type="checkbox"/>

☒ Include MSA Information View Query Information

Retrieve Tree(s) Remove Close



ToolBus

File Edit Help

Tools Views Groups

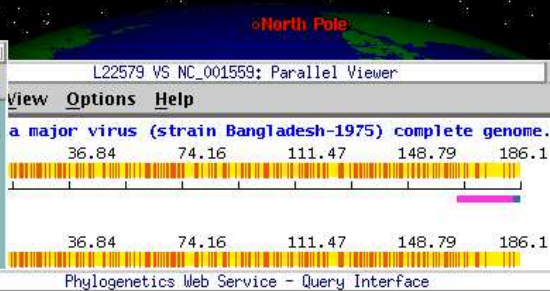
Web-Page URL Loader
Data: DNA - GenomeTool (beta)
Data: Organism - Pathogen Background Information
Data: Protein - Phylogenetic Trees (beta)
Data: Protein - Protein Interaction Pathways
DNA: Assembly - Contigs From Trace Files (restricted, beta)
DNA: Gene Prediction - Genscan (restricted, beta)
DNA: Gene Prediction - Glimmer (beta)
DNA: Gene Prediction - BDGF (restricted, beta)
DNA: Gene Prediction - GlimmerM (beta)
DNA: Gene Prediction - TigrScan (beta)
DNA: Gene Prediction - GrailEXP (restricted, beta)

Add Edit Use Remove

Active Tools

Tool	Status	Start
Data: Protein - Phylog...	Initialize	
Sequence: Alignment: ...	Completed 4/29/05 6:1	
Sequence: Search: Simi...	Completed 4/29/05 5:5	

Stop Reuse Info



Menu Database Help

Database "viral2" - Query Options

Species/Strains Descriptions About Database

List of 4164 genes/Annotations Selected genes/annotations

B19R	B26R
B1R	
B20R	
B21R	
B22R-LIKE PROTEIN	
B25R	
B26R	

Description key words: b26r Find

Submit Query Clear Query Update Jobs

Alignment Based Tree Information

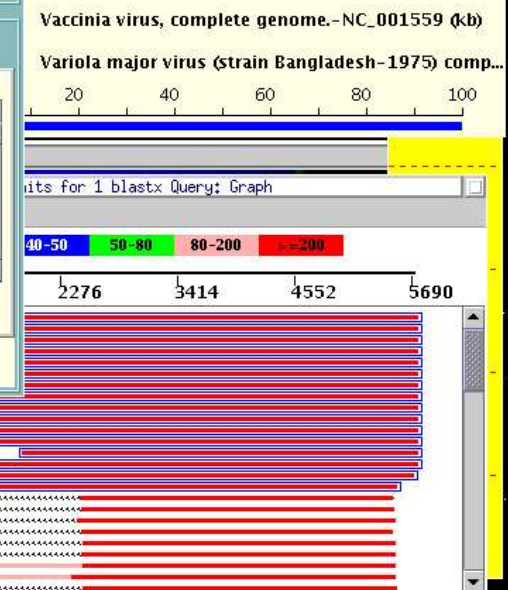
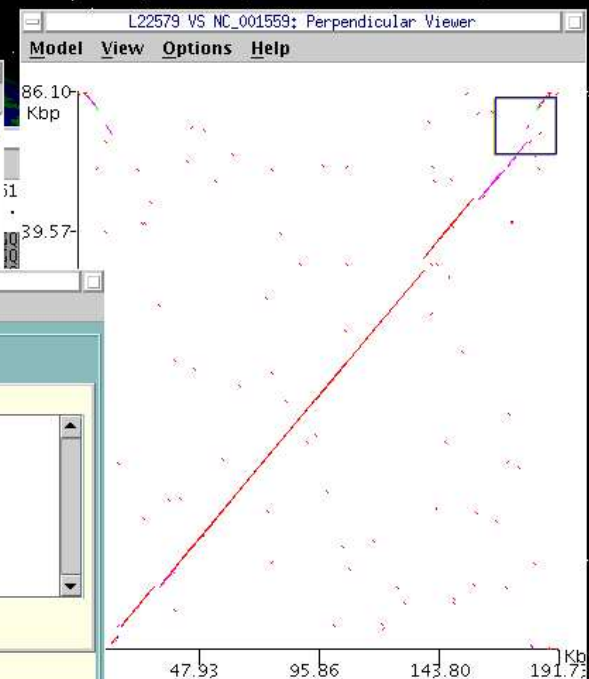
Query 1 Query 2

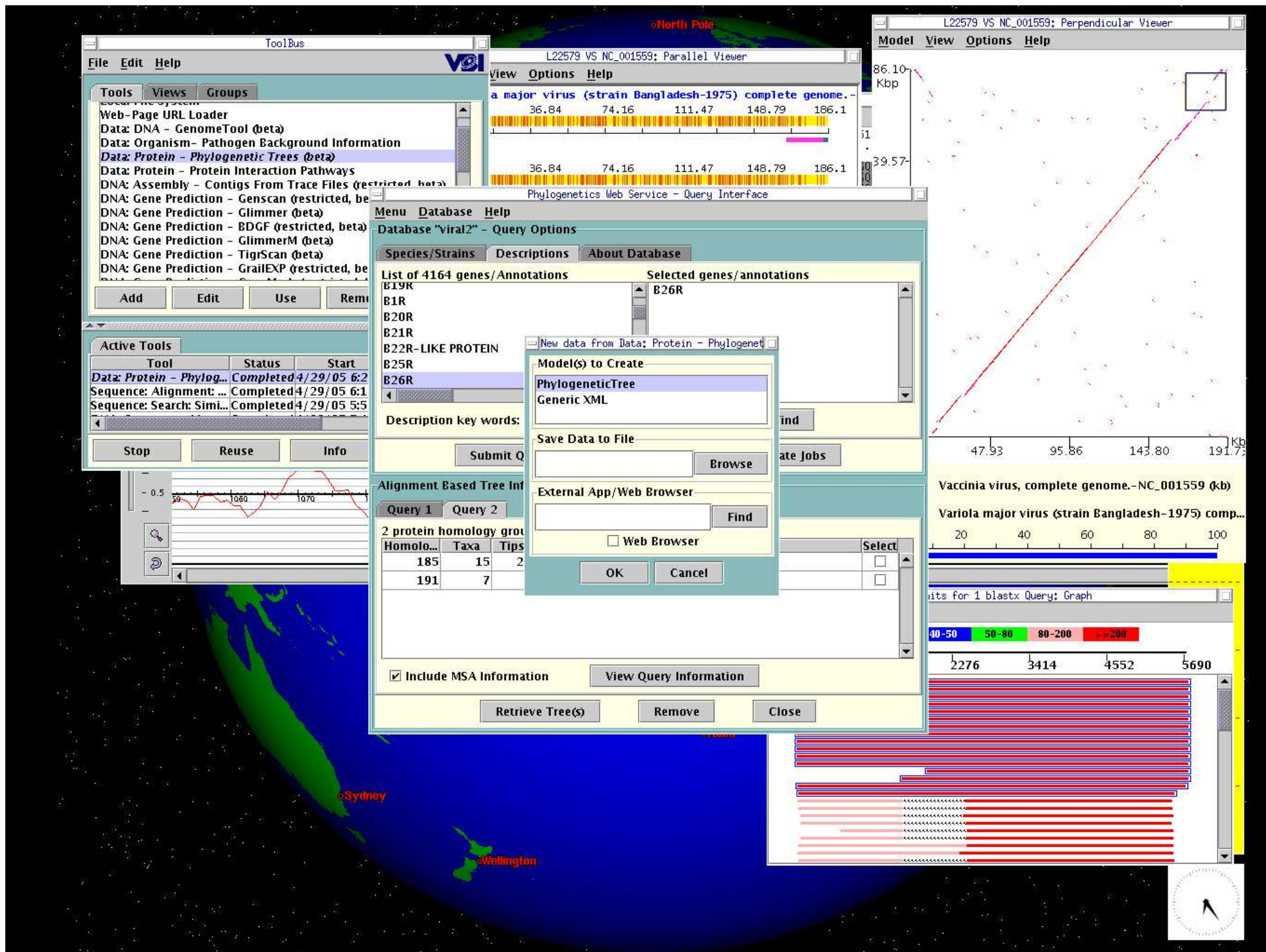
2 protein homology groups are shown for this query.

Homolo...	Taxa	Tips	Trees	Annotation	Select
185	15	25	2	B21R	<input type="checkbox"/>
191	7	7	1	B21R	<input type="checkbox"/>
				B22R-LIKE PROTEIN	<input type="checkbox"/>
				B26R	<input type="checkbox"/>
				C15R	<input type="checkbox"/>
				VAR B22R HOMOLOGUE	<input type="checkbox"/>
				VARIOLA B22R GENE FAMILY PROTEIN	<input type="checkbox"/>
				VARIOLA B22R-LIKE PROTEIN	<input type="checkbox"/>
				VARIOLA VIRUS B22R-LIKE PROTEIN	<input type="checkbox"/>

☒ Include MSA Information

Retrieve Tree(s) Remove Close





ToolBus

File Edit Help

Tools Views Groups

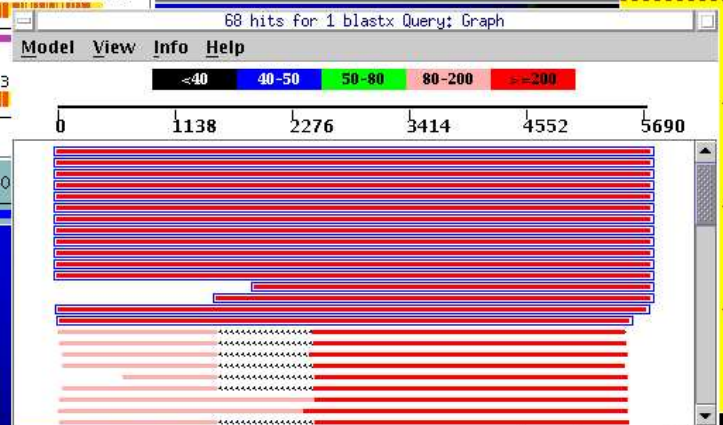
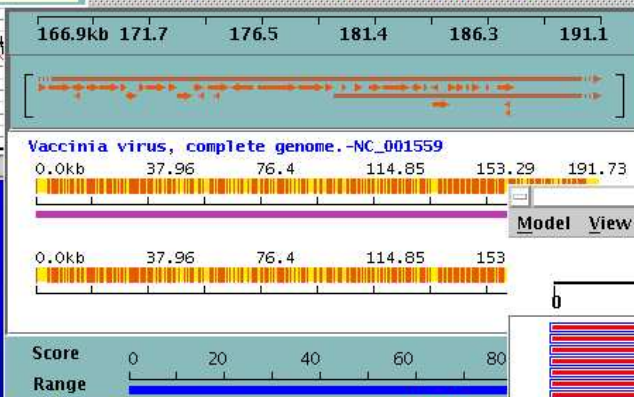
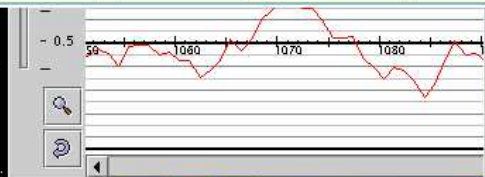
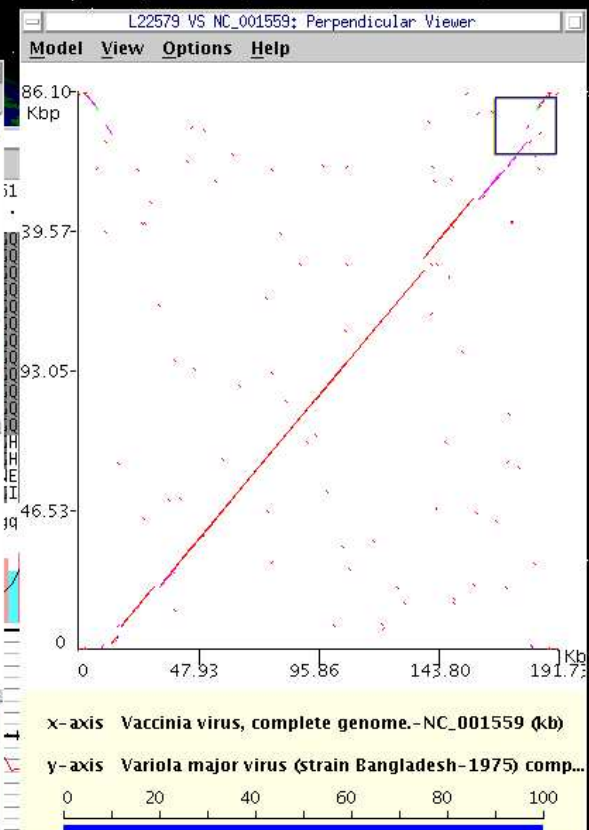
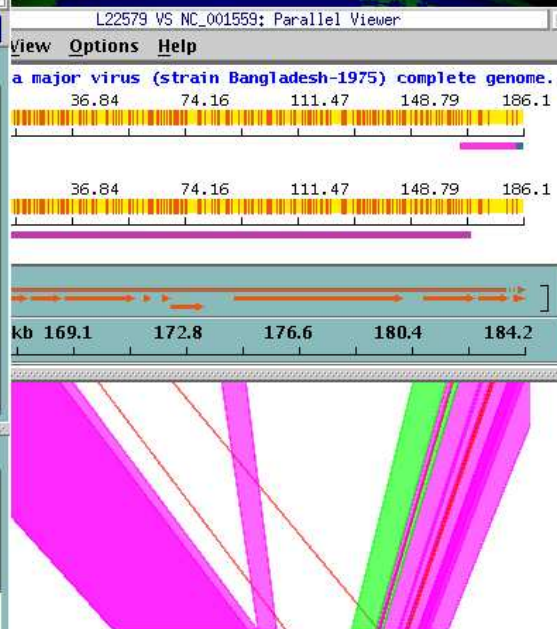
Web-Page URL Loader
 Data: DNA - GenomeTool (beta)
 Data: Organism - Pathogen Background Information
 Data: Protein - Phylogenetic Trees (beta)
 Data: Protein - Protein Interaction Pathways
 DNA: Assembly - Contigs From Trace Files (restricted, beta)
 DNA: Gene Prediction - Genscan (restricted, beta)
 DNA: Gene Prediction - Glimmer (beta)
 DNA: Gene Prediction - BDGF (restricted, beta)
 DNA: Gene Prediction - GlimmerM (beta)
 DNA: Gene Prediction - TigrScan (beta)
 DNA: Gene Prediction - GrailEXP (restricted, beta)

Add Edit Use Remove Find

Active Tools

Tool	Status	Start	Elapsed
Data: Protein - Phylog...	Completed	4/29/05 6:24 ...	00:00:03
Sequence: Alignment: ...	Completed	4/29/05 6:17 ...	00:01:16
Sequence: Search: Simi...	Completed	4/29/05 5:51 ...	00:02:26

Stop Reuse Info Delete



Phylogeny (1 alignments): Table

Model View Help

Alignment ID: 185

Topology ID	parsimony	likelihood
1467	6103	-32453
1468	6103	-32459



ToolBus

File Edit Help

Tools Views Groups

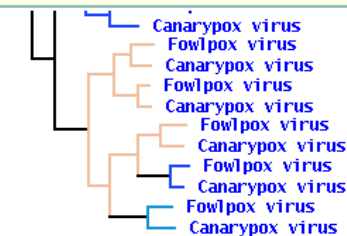
Web-Page URL Loader
 Data: DNA - GenomeTool (beta)
 Data: Organism - Pathogen Background Information
 Data: Protein - Phylogenetic Trees (beta)
 Data: Protein - Protein Interaction Pathways
 DNA: Assembly - Contigs From Trace Files (restricted, beta)
 DNA: Gene Prediction - Genscan (restricted, beta)
 DNA: Gene Prediction - Glimmer (beta)
 DNA: Gene Prediction - BDGF (restricted, beta)
 DNA: Gene Prediction - GlimmerM (beta)
 DNA: Gene Prediction - TigrScan (beta)
 DNA: Gene Prediction - GrailEXP (restricted, beta)

Add Edit Use Remove Find

Active Tools

Tool	Status	Start	Elap
Data: Organism - Path...	Initialize		
Data: Protein - Phylog...	Completed	4/29/05 6:24 ...	00:00
Sequence: Alignment: ...	Completed	4/29/05 6:17 ...	00:01

Stop Reuse Info



Alignment ID: 185
 Method: parsimony
 DB Name: viral2

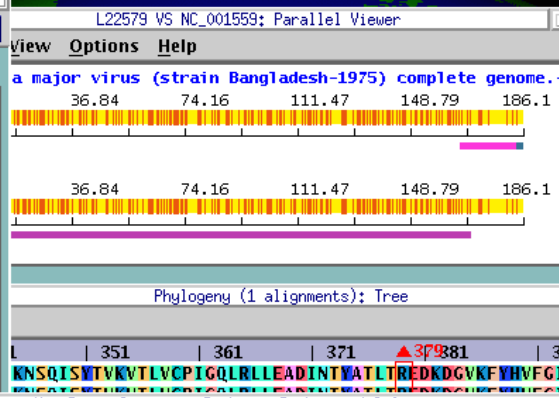
Topology ID: 1468
 Score: 6103
 Program Name: paup

Phylogeny (1 alignments): Table

Model View Help

Alignment ID: 185

Topology ID	parsimony	likelihood
1467	6103	-32453
1468	6103	-32459



Use Data: Organism - Pathogen Background Information

Data: Organism - Pathogen Background Information

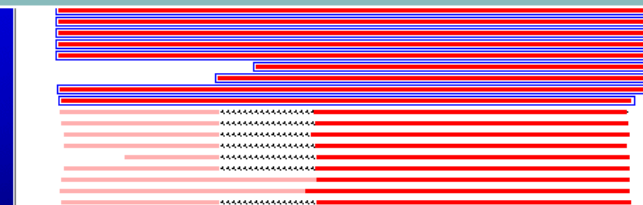
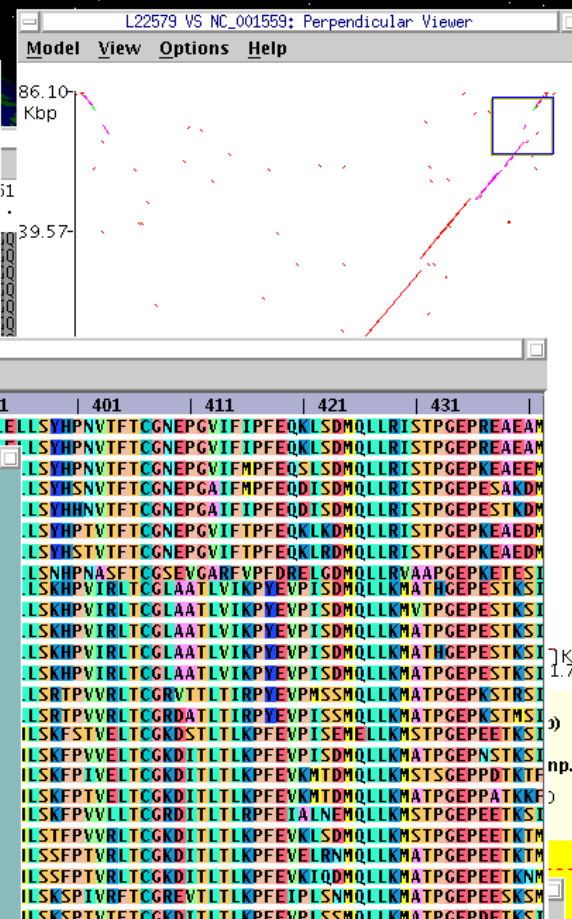
Retrieves a variety of background information for a select group of (mostly Human) pathogens.

runQuery

Burkholderia mallei
 Salmonella spp.
 Shigella spp.
 Variola Virus
 Venezuelan Equine Encephalitis Virus
 Yersinia pestis

Select species

Run Reset About Cancel



ToolBus

File Edit Help

Tools Views Groups

Web-Page URL Loader

Data: DNA - GenomeTool (beta)

Data: Organism - Pathogen Background Information

Data: Protein - Phylogenetic Trees (beta)

Data: Protein - Protein Interaction Pathways

DNA: Assembly - Contigs From Trace Files (restricted, beta)

DNA: Gene Prediction - Genscan (restricted, beta)

DNA: Gene Prediction - Glimmer (beta)

DNA: Gene Prediction - BDGF (restricted, beta)

DNA: Gene Prediction - GlimmerM (beta)

DNA: Gene Prediction - TigrScan (beta)

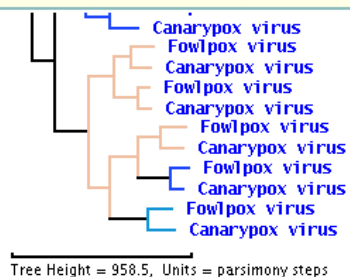
DNA: Gene Prediction - GrailEXP (restricted, beta)

Add Edit Use Remove Find

Active Tools

Tool	Status	Start	Elapsed
Data: Organism - Path...	Completed	4/29/05 6:30 ...	00:00:03
Data: Protein - Phylog...	Completed	4/29/05 6:24 ...	00:00:03
Sequence: Alignment: ...	Completed	4/29/05 6:17 ...	00:01:16

Stop Reuse Info Delete



Alignment ID: 185
Method: parsimony
DB Name: viral2

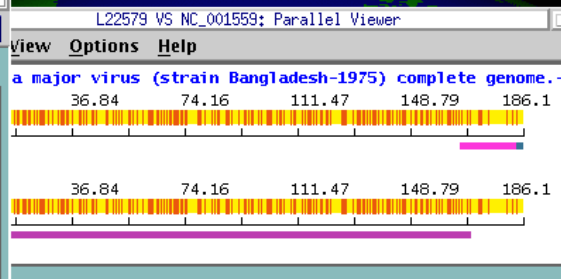
Topology ID: 1468
Score: 6103
Program Name: paup

Phylogeny (1 alignments): Table

Model View Help

Alignment ID: 185

Topology ID	parsimony	likelihood
1467	6103	-32453
1468	6103	-32459



Phylogeny (1 alignments): Tree

Model(s) to Create

Pathogen Background Information

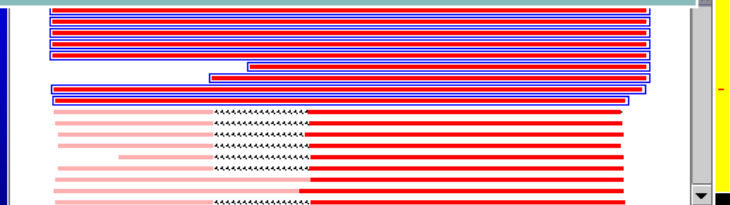
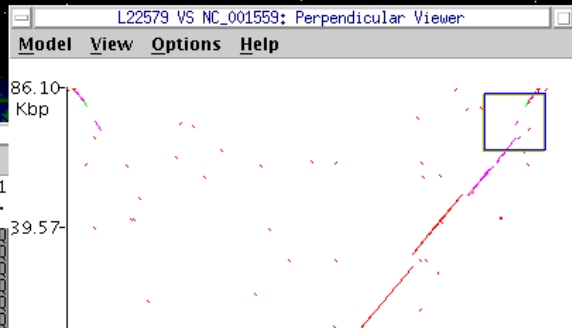
Generic XML

Save Data to File

External App/Web Browser

Web Browser

OK Cancel



Comparing Gene Expression After Infection by Ecoli, Influenza, Yeast

The Plasticity of Dendritic Cell Responses To Pathogens and Their Components.

Qian Huang, Dongyu Liu, Paul Majewski, Leah C. Schulte, Joshua M. Korn, Richard A. Young, Eric S. Lander & Nir Hacohen.
Science 294: 870-875 (2001)

ToolBus

File Edit Help

Tools Views Groups

Open File

- AAATicket
- Local File System
- Web-Page URL Loader
- Data: DNA - GenomeTool (beta)
- Data: Organism- Pathogen Background Information
- Data: Protein - Phylogenetic Trees (beta)
- Data: Protein - Protein Interaction Pathways
- DNA: Assembly - Contigs From Trace Files (restricted beta)
- DNA: Gen
- DNA: Gen
- DNA: Gen
- DNA: Gen

Model View Data Setting Help

No. of Genes: 4199 No. of Runs: 14

Add

Active To

Open File

Stop

Operations

Please click on the main categories on the left hand side panel to view a detailed list of operations in this panel.

Filter

Rows

Columns

Transform

Normalize

Clip Values

Log

Parameters

Please Drag and Drop Execution Units From The Operation F

KK << > X

Restore Original Data Undo Last Run Run Pipeline Delete Selected Item

Microarray: 14 runs on 4199 genes: Table

Id	fMed24r	hMed24r	iMed24r	mMed24r	tMed24r	feco24r	heco24r
X67325_at	0.0	0.0	0.0	0.0	0.0	3.7741394	2.821379
M97936_at	0.5785806	0.05798721	0.8586616	0.14464049	3.413126	1.4559742	2.447525
HG544-HT...	0.0	0.0	1.704748	0.0	4.5833335	2.7750857	4.0727806
V00594_at	0.0	0.0	0.0	0.0	0.0	6.5700984	6.2989125
U59286_at	0.0	0.0	0.0	0.0	0.0	0.0	0.0
X02530_at	0.0	0.6729445	0.0	0.26236424	0.4755969	1.2119409	0.6830968
U52513_at	0.0	0.0	0.8241754	-0.963174...	-0.418710...	2.6919208	3.90962
X64177_f_at	0.0	0.0	0.0	0.9400072	0.0	5.788675	5.558911
M65290_at	0.0	0.0	0.0	0.36464316	0.8001193	1.5347143	2.242835
M63573_at	-1.1939224	1.5686159	0.0	0.0	0.0	-1.1939224	1.3350011
U31628_at	0.0	0.0	0.0	0.0	0.0	2.3513753	2.9917243
HG3033-H...	-0.277631...	0.90825856	0.0	0.0	3.2898934	2.721096	0.0
Y08682_rn...	0.0	0.88376755	0.0	0.9555114	3.6022317	0.0	0.47000363
M33882_at	0.0	0.0	0.0	0.0	-1.5204904	2.5587766	4.067316
U22662_at	0.0	1.4997947	0.10008342	-0.198850...	3.295837	0.0	2.5530446
S57235_at	-1.2697606	2.7474918	1.194113	1.5835322	5.655992	-1.2697606	0.7386479
AFFX-HUM...	1.708182	2.8746939	0.15266365	1.4284859	4.6662655	0.4144338	0.6830968
M13755_at	0.7613554	0.0	-0.320167...	0.18551388	1.8510243	4.262514	5.7594695
HG2724-H...	0.0	0.0	0.0	0.0	0.0	0.0	0.0
M21121_at	-0.095310...	0.0	0.0	0.981748	1.7792139	5.1606216	5.733406
M24594_at	0.0582688...	0.0	0.0	-0.3364722	0.42683998	1.0006319	3.1415627
U77180_at	0.0	0.0	0.0	0.0	0.0	1.5518087	0.0
D38128_at	0.0	0.0	0.0	0.0	0.0	1.0851892	2.1494339
AB000115...	0.59883654	-0.564116...	0.8586616	0.49469623	2.3413584	1.1878434	1.1358349
M59815_at	0.0	0.0	0.0	0.6199826	3.8321135	0.30748472	0.0
X07834_at	0.0	0.0	0.01980261	-0.2638146	1.0833448	2.6810215	3.640739
X72755_at	0.0392206...	0.35086098	0.8754688	-0.3220835	0.44084707	1.7119945	0.24323036
U20647_at	0.01980261	0.0582688...	0.1655144	-0.457424...	3.2665224	0.5653138	1.7119945
X87344_cd...	-1.8148248	1.4357067	1.9691463	3.430756	4.4575977	-1.8148248	-1.1184149
X78706_at	-0.985816...	0.0	0.0	0.7099948	3.6908774	0.565992	0.0
U84720_at	0.4462871	1.5633202	1.4492692	1.7544037	4.3153524	-0.940007...	0.15616074
AFFX-HUM...	2.089392	3.0204248	0.7393157	1.1381356	4.8562403	1.6486586	0.0
U19523_at	0.0	0.0	0.0	0.0	-0.6830969	1.258461	2.2148461
U37518_at	0.0	0.0	0.0	0.0	-0.434214...	1.7647308	2.5241272
M54915_s...	0.10389962	0.34174928	0.28347158	-0.560502...	3.1072736	1.6108967	2.0682683
D84276_at	0.0	0.0	0.0	0.0	-0.364897...	1.6331544	3.3061538
J05582_s_at	0.0	0.0	0.0	0.8329091	0.0	0.6830968	0.0
J04164_at	1.8870696	1.8594182	1.798404	2.0122328	1.378742	4.5999565	4.9991026
M28170_at	0.0	0.3920421	0.0	0.45953235	3.18387	0.0	0.0582688...
U72882_s...	0.7006944	-0.031090...	-0.307484...	-0.540384...	0.11984403	2.304099	2.7795796
X67325_at	0.4446405	0.8586616	0.8586616	0.55707242	1.3813810	0.4446405	1.3144442

Data distribution Compare two runs

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Microarray: 1

ToolBus

File Edit Help

Tools Views Groups

Open File
AAATicket
Local File System
Web-Page URL Loader
Data: DNA - GenomeTool (beta)
Data: Organism- Pathogen Background Information
Data: Protein - Phylogenetic Trees (beta)
Data: Protein - Protein Interaction Pathways
DNA: Assembly - Contigs From Trace Files (restricted beta)
DNA: Gen
DNA: Gen Model View Data Setting Help
DNA: Gen
DNA: Gen

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Please Drag and Drop Execution Units From The Operation F

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Restore Original Data Undo Last Run Run Pipeline Delete Selected Item C Pip

Microarray: 14 runs on 4199 genes: Table

Id	fMed24r	hMed24r	iMed24r	mMed24r	tMed24r	feco24r	heco24r
X67325_at	0.0	0.0	0.0	0.0	0.0	3.7741394	2.821379
M97936_at	0.5785806	0.05798721	0.8586616	0.14464049	3.413126	1.4559742	2.447525
HG544-HT...	0.0	0.0	1.704748	0.0	4.5833335	2.7750857	4.0727806
V00594_at	0.0	0.0	0.0	0.0	0.0	6.5700984	6.2989125
U59286_at	0.0	0.0	0.0	0.0	0.0	0.0	0.0
X02530_at	0.0	0.6729445	0.0	0.26236424	0.4755969	1.2119409	0.6830968
U52513_at	0.0	0.0	0.8241754	-0.963174...	-0.418710...	2.6919208	3.90962
X64177_f_at	0.0	0.0	0.0	0.9400072	0.0	5.788675	5.558911
M65290_at	0.0	0.0	0.0	0.36464316	0.8001193	1.5347143	2.242835
M63573_at	-1.1939224	1.5686159	0.0	0.0	0.0	-1.1939224	1.3350011
U31628_at	0.0	0.0	0.0	0.0	0.0	2.3513753	2.9917243
HG3033-H...	-0.277631...	0.90825856	0.0	0.0	3.2898934	2.721096	0.0
Y08682_rn...	0.0	0.88376755	0.0	0.9555114	3.6022317	0.0	0.47000363
M33882_at	0.0	0.0	0.0	0.0	-1.5204904	2.5587766	4.067316
U22662_at	0.0	1.4997947	0.10008342	-0.198850...	3.295837	0.0	2.5530446
S57235_at	-1.2697606	2.7474918	1.194113	1.5835322	5.655992	-1.2697606	0.7386479
AFFX-HUM...	1.708182	2.8746939	0.15266365	1.4284859	4.6662655	0.4144338	0.6830968
M13755_at	0.7613554	0.0	-0.320167...	0.18551388	1.8510243	4.262514	5.7594695
HG2724-H...	0.0	0.0	0.0	0.0	0.0	0.0	0.0
M21121_at	-0.095310...	0.0	0.0	0.981748	1.7792139	5.1606216	5.733406
M24594_at	0.0582688...	0.0	0.0	-0.3364722	0.42683998	1.0006319	3.1415627
U77180_at	0.0	0.0	0.0	0.0	0.0	1.5518087	0.0
D38128_at	0.0	0.0	0.0	0.0	0.0	1.0851892	2.1494339
AB000115...	0.59883654	-0.564116...	0.8586616	0.49469623	2.3413584	1.1878434	1.1358349
M59815_at	0.0	0.0	0.0	0.6199826	3.8321135	0.30748472	0.0
X07834_at	0.0	0.0	0.01980261	-0.2638146	1.0833448	2.6810215	3.640739
X72755_at	0.0392206...	0.35086098	0.8754688	-0.3220835	0.44084707	1.7119945	0.24323036
U20647_at	0.01980261	0.0582688...	0.1655144	-0.457424...	3.2665224	0.5653138	1.7119945
X87344_cd...	-1.8148248	1.4357067	1.9691463	3.430756	4.4575977	-1.8148248	-1.1184149
X78706_at	-0.985816...	0.0	0.0	0.7099948	3.6908774	0.565992	0.0
U84720_at	0.4462871	1.5633202	1.4492692	1.7544037	4.3153524	-0.940007...	0.15616074
AFFX-HUM...	2.089392	3.0204248	0.7393157	1.1381356	4.8562403	1.6486586	0.0
U19523_at	0.0	0.0	0.0	0.0	-0.6830969	1.258461	2.2148461
U37518_at	0.0	0.0	0.0	0.0	-0.434214...	1.7647308	2.5241272
M54915_s...	0.10389962	0.34174928	0.28347158	-0.560502...	3.1072736	1.6108967	2.0682683
D84276_at	0.0	0.0	0.0	0.0	-0.364897...	1.6331544	3.3061538
J05582_s...	0.0	0.0	0.0	0.8329091	0.0	0.6830968	0.0
J04164_at	1.8870696	1.8594182	1.798404	2.0122328	1.378742	4.5999565	4.9991026
M28170_at	0.0	0.3920421	0.0	0.45953235	3.18387	0.0	0.0582688...
U72882_s...	0.7006944	-0.031090...	-0.307484...	-0.540384...	0.11984403	2.304099	2.7795796
X67325_at	0.0	0.0	0.0	0.0	0.0	0.0	0.0

Data distribution Compare two runs

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Microarray: 1

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File Edit Help

Tools Views Groups

Open File
AAATicket
Local File System
Web-Page URL Loader
Data: DNA - GenomeTool (beta)
Data: Organism- Pathogen Background Information
Data: Protein - Phylogenetic Trees (beta)
Data: Protein - Protein
DNA: Assembly
DNA: Gen
DNA: Gen
DNA: Gen
DNA: Gen

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Stop

Filter
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Clip Values
Log
Parameters

Model View Data Select Help

Model View

Please select ONE

Existing Results:

Analysis Services:

t/f-test

Row selection ☒ All rows ☐ Selected rows (0 out of 4199)

Add Factor

List View

Tree View

All Factors

Columns for t/f test

fMed24r
hMed24r
iMed24r
mMed24r
tMed24r

V/S

feco24r
heco24r
tEco24r

Apply

Cancel

Please Drag and Drop Execution Units From The Operation F

KK

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Restore
Original
Data

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Last
Run

Run
Pipeline

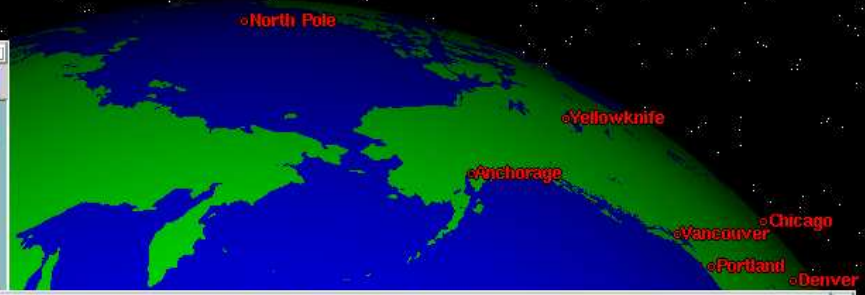
Delete
Selected
Item

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Pip

U19523_at	0.0	0.0	0.0	0.0	-0.6830969	1.258461	2.2148461
U37518_at	0.0	0.0	0.0	0.0	-0.434214...	1.7647308	2.5241272
M54915_s...	0.10389962	0.34174928	0.28347158	-0.560502...	3.1072736	1.6108967	2.0682683
D84276_at	0.0	0.0	0.0	0.0	-0.364897...	1.6331544	3.3061538
J05582_s_at	0.0	0.0	0.0	0.8329091	0.0	0.6830968	0.0
J04164_at	1.8870696	1.8594182	1.798404	2.0122328	1.378742	4.5999565	4.9991026
M28170_at	0.0	0.3920421	0.0	0.45953235	3.18387	0.0	0.0582688...
U72882_s...	0.7006944	-0.031090...	-0.307484...	-0.540384...	0.11984403	2.304099	2.7795796
VE7251...	0.4446958	0.8637632	0.8587688	0.55707342	1.3813810	0.4446958	1.3144442
Id							

Data distribution

Compare two runs



Microarray: 14 runs on 4199 genes: t/f-test

heco24r

2.821379
2.447525
4.0727806
6.2989125
0.0
0.6830968
3.90962
5.558911
2.242835
1.3350011
2.9917243
0.0
0.47000363
4.067316
2.5530446
0.7386479
0.6830968
5.7594695
0.0
5.733406
3.1415627
0.0
2.1494339
1.1358349
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3.640739
0.24323036
1.7119945
-1.1184149
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0.15616074
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ToolB

Microarray41



ToolBus

File Edit Help

Tools Views Groups

Open File
AAATicket
Local File System
Web-Page URL Loader
Data: DNA - GenomeTool (beta)
Data: Organism- Pathogen Background Information
Data: Protein - Phylogenetic Trees (beta)
Data: Protein - Protein
DNA: Assembly
DNA: Gen
DNA: Gen
DNA: Gen
DNA: Gen

Add

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Stop

Filter

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Transform
Normalize
Clip Values
Log

Parameters

Please Drag and Drop Execution Units From The Operation F

KK << > X

Restore Original Data Undo Last Run Run Pipeline Delete Selected Item

Microarray: 14 runs on 4199 genes: t/f-test

Model View Data Select Help

Table Text Graphic

	2(Mean)	2(Median)	2(Sd)	1(Mean)	1(Median)	1(Sd)
X67325_at	4.3832264	3.7741394	1.939...	0.0	0.0	0.0
X67325_at	4.3832264	3.7741394	1.939...	0.0	0.0	0.0
V00594_at	6.6052585	6.5700984	0.325...	0.0	0.0	0.0
U52513_at	3.9424527	3.90962	1.267...	-0.1115...	0.0	0.6
X64177_f_at	5.9972816	5.788675	0.571...	0.18800...	0.0	0.4
U31628_at	3.5356774	2.9917243	1.530...	0.0	0.0	0.0
M33882_at	3.5719252	4.067316	0.877...	-0.3040...	0.0	0.6
M13755_at	4.8369412	4.48884	0.806...	0.4955452	0.18551388	0.8
M21121_at	5.095624	5.1606216	0.672...	0.53313...	0.0	0.8
M24594_at	2.577417	3.1415627	1.383...	0.02972...	0.0	0.2
X07834_at	3.6213446	3.640739	0.930...	0.16786...	0.0	0.5
U19523_at	2.303191	2.2148461	1.091...	-0.1366...	0.0	0.3
U37518_at	2.5421808	2.5241272	0.786...	-0.0868...	0.0	0.1
D84276_at	2.939743	3.3061538	1.167...	-0.0729...	0.0	0.1
J04164_at	4.460128	4.5999565	0.620...	1.7871733	1.8594182	0.2
U72882_s_at	2.8696487	2.7795796	0.615...	-0.0116...	-0.0310905...	0.4
U53830_at	3.117777	3.3297114	0.628...	-0.5502...	0.0	1.0
X04602_s_at	4.48491	4.2183304	0.934...	-0.1048...	0.0	0.5
U22970_rna...	3.0750666	3.676807	1.243...	0.4029806	0.0	0.9
M13690_s_at	2.8020205	2.8061113	0.040...	0.40825...	0.59883654	0.3
U88964_at	3.7971723	3.7025385	0.492...	0.8955889	0.8398002	0.3
M72885_rna...	3.1140747	3.0791538	0.644...	-0.764915	0.0	1.1

es: Table

	iMed24r	mMed24r	tMed24r	feco24r	heco24r
98721	0.8586616	0.14464049	3.413126	1.4559742	2.447525
	1.704748	0.0	4.5833335	2.7750857	4.0727806
	0.0	0.0	0.0	6.5700984	6.2989125
	0.0	0.0	0.0	0.0	0.0
9445	0.0	0.26236424	0.4755969	1.2119409	0.6830968
	0.8241754	-0.963174...	-0.418710...	2.6919208	3.90962
	0.0	0.9400072	0.0	5.788675	5.558911
	0.0	0.36464316	0.8001193	1.5347143	2.242835
6159	0.0	0.0	0.0	-1.1939224	1.3350011
	0.0	0.0	0.0	2.3513753	2.9917243
25856	0.0	0.0	3.2898934	2.721096	0.0
76755	0.0	0.9555114	3.6022317	0.0	0.47000363
	0.0	0.0	-1.5204904	2.5587766	4.067316
7947	0.10008342	-0.198850...	3.295837	0.0	2.5530446
4918	1.194113	1.5835322	5.655992	-1.2697606	0.7386479
6939	0.15266365	1.4284859	4.6662655	0.4144338	0.6830968
	-0.320167...	0.18551388	1.8510243	4.262514	5.7594695
	0.0	0.0	0.0	0.0	0.0
	0.0	0.981748	1.7792139	5.1606216	5.733406
	0.0	-0.3364722	0.42683998	1.0006319	3.1415627
	0.0	0.0	1.5518087	0.0	0.0
	0.0	0.0	0.0	1.0851892	2.1494339
	0.0	0.0	0.0	1.1878434	1.1358349
	0.0	0.6199826	3.8321135	0.30748472	0.0
X07834_at	0.0	0.0	0.01980261	-0.2638146	1.0833448
X72755_at	0.0392206...	0.35086098	0.8754688	-0.3220835	0.44084707
U20647_at	0.01980261	0.0582688...	0.1655144	-0.457424...	3.2665224
X87344_cd...	-1.8148248	1.4357067	1.9691463	3.430756	4.4575977
X78706_at	-0.985816...	0.0	0.0	0.7099948	3.6908774
U84720_at	0.4462871	1.5633202	1.4492692	1.7544037	4.3153524
AFFX-HUM...	2.089392	3.0204248	0.7393157	1.1381356	4.8562403
U19523_at	0.0	0.0	0.0	0.0	-0.6830969
U37518_at	0.0	0.0	0.0	0.0	-0.434214...
M54915_s...	0.10389962	0.34174928	0.28347158	-0.560502...	3.1072736
D84276_at	0.0	0.0	0.0	0.0	-0.364897...
J05582_s_at	0.0	0.0	0.0	0.8329091	0.0
J04164_at	1.8870696	1.8594182	1.798404	2.0122328	1.378742
M28170_at	0.0	0.3920421	0.0	0.45953235	3.18387
U72882_s...	0.7006944	-0.031090...	-0.307484...	0.11984403	2.304099
X67325_at	0.4446858	0.8637627	0.8586616	0.55707242	1.2812810

Data distribution

Compare two runs


Desk 0

XU col

City

ToolB

Microarray: 1



ToolBus

File Edit Help

Tools Views Groups

Selected Items

New

Active To

Statistic Ar

Open File

Stop

Filter

Rows

Columns

Transform

Normalize

Clip Values

Log

Microarray: 14 runs on 4199 genes; t/f-test

Model	View	Data	Select	Help
Select All				
De-Select All		Ctrl-D		
Export Model Data		Ctrl-E		
Edit Model Tools				
Remove Model		Ctrl-R		
Create Group		Ctrl-G		
ToolBus to Front		Ctrl-T		

Model	View	Data	Select	Help		
Model	View	Score	Pvalue	Significant		
803	0.410...	-3.53...	0.0062...	TRUE		
8077	0.376...	-5.80...	2.801E...	TRUE		
59	0.422...	-2.94...	0.03379	TRUE		
081	0.651...	10.19...	0.0	TRUE		
731	0.753...	-3.72...	0.0034...	TRUE		
06	1.381...	1.562...	0.4264	FALSE		
	2.000...	2.380...	0.1186	FALSE		
1.419...	0.0	0.0	0.0	FALSE		
1.506...	0.2821811	0.26236424	0.295...	1.729...	0.3461	FALSE
1.942...	0.23295...	0.0	0.354...	2.435...	0.1079	FALSE
2.007...	0.0749387	0.0	0.982...	0.722...	0.7739	FALSE
2.284...	0.78410...	0.0	1.470...	1.109...	0.6207	FALSE
1.870...	1.0883021	0.88376755	1.478...	0.172...	0.9589	FALSE
1.718...	0.93937...	0.10008342	1.478...	0.839...	0.7253	FALSE
2.183...	1.9822737	1.5835322	2.521...	-0.66...	0.799	FALSE
1.454...	2.1660583	1.708182	1.700...	-0.68...	0.7923	FALSE
2.069...	0.0	0.0	0.0	1.0	0.6544	FALSE
2.695...	0.0	0.0	0.0	1.456...	0.4772	FALSE
1.726...	0.0	0.0	0.0	2.573...	0.08204	FALSE
1.376...	0.74588...	0.59883654	1.043...	1.313...	0.5324	FALSE
1.967...	0.89041...	0.0	1.666...	0.291...	0.9271	FALSE

Parameters

Please Drag and Drop Execution Units From The Operation F

KK	<<	>	X	
Restore Original Data	Undo Last Run	Run Pipeline	Delete Selected Item	

AB000115...	0.59883654	-0.5
M59815_at	0.0	0.0
X07834_at	0.0	0.0
X72755_at	0.0392206...	0.35
U20647_at	0.01980261	0.05
X87344_cd...	-1.8148248	1.43
X78706_at	-0.985816...	0.0
U84720_at	0.4462871	1.56
AFFX-HUM...	2.089392	3.02
U19523_at	0.0	0.0
U37518_at	0.0	0.0
M54915_s...	0.10389962	0.34
D84276_at	0.0	0.0
J05582_s_at	0.0	0.0
J04164_at	1.8870696	1.85
M28170_at	0.0	0.39
U72882_s...	0.7006944	-0.0
X57351_at	0.4446858	0.86
Id		

Data distrib

North Pole

Yellowknife

Wichorage

Vancouver

Chicago

Portland

Denver

es; Table

ed24r	iMed24r	mMed24r	tMed24r	feco24r	heco24r
0.0	0.0	0.0	0.0	3.7741394	2.821379
98721	0.8586616	0.14464049	3.413126	1.4559742	2.447525
	1.704748	0.0	4.5833335	2.7750857	4.0727806
	0.0	0.0	0.0	4.7700884	4.7980125
	0.0	0.0	0.0	0.0	0.0
9445	0.0	0.26236424	0.4755969	1.2119409	0.6830968
	0.8241754	-0.963174...	-0.418710...	2.6919208	3.90962
	0.0	0.9400072	0.0	5.788675	5.558911
	0.0	0.36464316	0.8001193	1.5347143	2.242835
6159	0.0	0.0	0.0	-1.1939224	1.3350011
	0.0	0.0	0.0	2.3513753	2.9917243
25856	0.0	0.0	3.2898934	2.721096	0.0
76755	0.0	0.9555114	3.6022317	0.0	0.47000363
	0.0	-1.5204904	2.5587766	4.067316	
7947	0.10008342	-0.198850...	3.295837	0.0	2.5530446
4918	1.194113	1.5835322	5.655992	-1.2697606	0.7386479
6939	0.15266365	1.4284859	4.6662655	0.4144338	0.6830968
	-0.320167...	0.18551388	1.8510243	4.262514	5.7594695
	0.0	0.0	0.0	0.0	0.0
	0.0	0.981748	1.7792139	5.1606216	5.734886
	0.0	-0.3364722	0.42683998	1.0006319	3.1415627
	0.0	0.0	0.0	1.5518087	0.0
	0.0	0.0	0.0	1.0851892	2.1494339
	0.0	0.0	0.0	1.1878434	1.1358349
	0.0	0.6199826	3.8321135	0.30748472	0.0
	0.01980261	-0.2638146	1.0833448	2.6810215	3.640739
X72755_at	0.0392206...	0.35086098	0.8754688	-0.3220835	0.44084707
U20647_at	0.01980261	0.0582688...	0.1655144	-0.457424...	3.2665224
X87344_cd...	-1.8148248	1.4357067	1.9691463	3.430756	4.4575977
X78706_at	-0.985816...	0.0	0.0	0.7099948	3.6908774
U84720_at	0.4462871	1.5633202	1.4492692	1.7544037	4.3153524
AFFX-HUM...	2.089392	3.0204248	0.7393157	1.1381356	4.8562403
U19523_at	0.0	0.0	0.0	0.0	-0.6830969
U37518_at	0.0	0.0	0.0	0.0	-0.434214...
M54915_s...	0.10389962	0.34174928	0.28347158	-0.560502...	3.1072736
D84276_at	0.0	0.0	0.0	0.0	-0.364897...
J05582_s...	0.0	0.0	0.0	0.8329091	0.0
J04164_at	1.8870696	1.8594182	1.798404	2.0122328	1.378742
M28170_at	0.0	0.3920421	0.0	0.45953235	3.18387
U72882_s...	0.7006944	-0.031090...	-0.307484...	-0.540384...	0.11984403
U72751...	0.4416958	0.8637632	0.0597688	0.55707342	1.2813810
	0.4416958	0.8637632	0.0597688	0.55707342	1.2813810

Data distribution

Compare two runs

Desk 0

XU co

ToolBus

Microarray: 1

Microarray: 1

Microarray: 1

ToolBus

File Edit Help

Tools Views Groups

Selected Items

Microarray: 14 runs on 4199 genes (ecoli) (Microarray: 14 runs...)

Microarray: 14 runs on 4199 genes (flu) (Microarray: 14 runs o...)

New Edit

Active Tools

Tool

Statistic Analysis (T-t...)

Open File

Stop Rel

Rows Columns

Transform

Normalize

Clip Values

Log

Parameters

Please Drag and Drop Execution Units From The Operation F

KK << > X

Restore Original Data Undo Last Run Run Pipeline Delete Selected Item

Microarray: 14 runs on 4199 genes: t/f-test2

Model View Data Select Help

Table Text Graphic

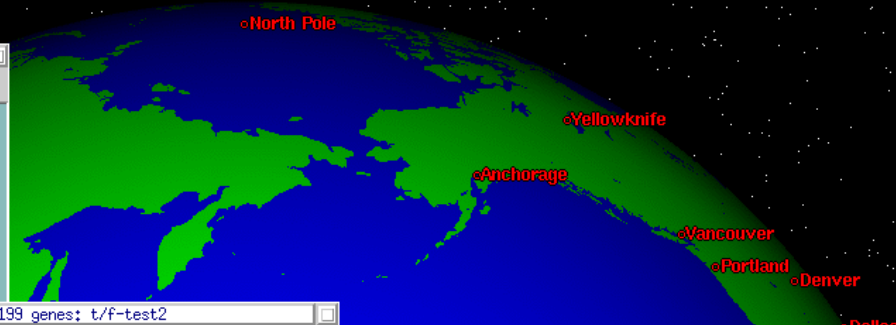
2(Sd)	1(Mean)	1(Median)	1(Sd)	Score	Pvalue	Significant
0.374...	-0.0213...	0.10536056	0.343...	-5.92...	2.099E...	TRUE
0.571...	0.0738705	0.020619325	0.419...	-8.08...	9.022E...	TRUE
0.537...	0.09141...	0.0614987	0.297...	-3.69...	0.0045...	TRUE
0.261...	-0.1769...	-0.12456271	0.312...	-4.08...	0.0011...	TRUE
0.598...	-0.3077...	-0.26246506	0.351...	-3.64...	0.0054...	TRUE
0.136...	-0.4747...	-0.6480267	0.964...	3.179...	0.02172	TRUE
0.220...	0.04552...	-0.07207237	0.193...	-12.3...	0.0	TRUE
0.202...	-0.0276...	0.07410803	0.410...	-3.52...	0.0076...	TRUE
0.361...	-0.0491...	-0.18728077	0.376...	-7.14...	9.76E...	TRUE
0.017...	0.34361...	0.41871032	0.219...	-3.58...	0.0064...	TRUE
0.367...	-0.8303...	-0.7953531	0.778...	-2.98...	0.03763	TRUE
1.821...	1.0105991	0.5785806	1.381...	1.387...	0.6204	FALSE
0.550...	1.2576163	0.0	2.000...	2.407...	0.1469	FALSE
0.798...	0.23295...	0.0	0.354...	0.467...	0.9271	FALSE
1.150...	0.0749387	0.0	0.982...	1.013...	0.7733	FALSE
1.653...	0.0	0.0	0.0	1.823...	0.3931	FALSE
2.531...	0.78410...	0.0	1.470...	0.334...	0.9444	FALSE
1.573...	1.0883021	0.88376755	1.478...	0.850...	0.8343	FALSE
1.478...	1.9822737	1.5835322	2.521...	-1.53...	0.5432	FALSE
2.659...	2.1660583	1.708182	1.700...	0.219	0.9609	FALSE
1.688...	0.0	0.0	0.0	1.0	0.7733	FALSE

AB000115...	0.59883654	-0.564116...	0.8586616	0.49469623	2.3413584	1.1878434	1.1358349
M59815_at	0.0	0.0	0.0	0.6199826	3.8321135	0.30748472	0.0
X07834_at	0.0	0.0	0.01980261	-0.2638146	1.0833448	2.6810215	3.640739
X72755_at	0.0392206...	0.35086098	0.8754688	-0.3220835	0.44084707	1.7119945	0.24323036
U20647_at	0.01980261	0.0582688...	0.1655144	-0.457424...	3.2665224	0.5653138	1.7119945
X87344_cd...	-1.8148248	1.4357067	1.9691463	3.430756	4.4575977	-1.8148248	-1.1184149
X78706_at	-0.985816...	0.0	0.0	0.7099948	3.6908774	0.565992	0.0
U84720_at	0.4462871	1.5633202	1.4492692	1.7544037	4.3153524	-0.940007...	0.15616074
AFFX-HUM...	2.089392	3.0204248	0.7393157	1.1381356	4.8562403	1.6486586	0.0
U19523_at	0.0	0.0	0.0	0.0	-0.6830969	1.258461	2.2148461
U37518_at	0.0	0.0	0.0	0.0	-0.434214...	1.7647308	2.5241272
M54915_s...	0.10389962	0.34174928	0.28347158	-0.560502...	3.1072736	1.6108967	2.0682683
D84276_at	0.0	0.0	0.0	0.0	-0.364897...	1.6331544	3.3061538
J05582_s...	0.0	0.0	0.0	0.8329091	0.0	0.6830968	0.0
J04164_at	1.8870696	1.8594182	1.798404	2.0122328	1.378742	4.5999565	4.9991026
M28170_at	0.0	0.3920421	0.0	0.45953235	3.18387	0.0	0.0582688...
U72882_s...	0.7006944	-0.031090...	-0.307484...	-0.540384...	0.11984403	2.304099	2.7795796
X57251...	0.4446958	0.8637637	0.8593698	0.55707342	1.2812810	0.4446958	1.3144443

Id

Data distribution

Compare two runs



Desk 0

XU co

City

ToolBus

Microarray: 1

ToolBus

File Edit Help

Tools Views Groups

Selected Items

Microarray: 14 runs on 4199 genes (ecoli) (Microarray: 14 runs...
Microarray: 14 runs on 4199 genes (flu) (Microarray: 14 runs o...

New

Active To

Statistic Ar

Open File

Stop

Filter

Rows

Columns

Transform

Normalize

Clip Values

Log

Parameters

Model View Data Select Help

Please select ONE

Existing Results:

Statistics test 1, type: two-sample Welch t-statistics (unequal ...
Statistics test 2, type: two-sample Welch t-statistics (unequal ...

Analysis Services:

t/f-test

Row selection ☒ All rows ☐ Selected rows (0 out of 4199)

Add Factor

List View

Column ID	Factor:1
iMed24r	
mMed24r	
tMed24r	
feco24r	
heco24r	
tEco24r	
fPr824r	
tPr824r	
hPr824r	
iCan24r	
mcan24r	
tcan24r	

Tree View

- All Factors
 - Factor:1

Columns for t/f test

fMed24r
hMed24r
iMed24r
mMed24r
tMed24r

V/S

iCan24r
mcan24r
tcan24r

Apply Cancel

Please Drag and Drop Execution Units From The Operation F

Id	0.4446958	0.8637632	0.8587688	0.55707342	1.2813810	0.4446958	1.3144442
U19523_at	0.0	0.0	0.0	0.0	-0.6830969	1.258461	2.2148461
U37518_at	0.0	0.0	0.0	0.0	-0.434214...	1.7647308	2.5241272
M54915_s...	0.10389962	0.34174928	0.28347158	-0.560502...	3.1072736	1.6108967	2.0682683
D84276_at	0.0	0.0	0.0	0.0	-0.364897...	1.6331544	3.3061538
J05582_s_at	0.0	0.0	0.0	0.8329091	0.0	0.6830968	0.0
J04164_at	1.8870696	1.8594182	1.798404	2.0122328	1.378742	4.5999565	4.9991026
M28170_at	0.0	0.3920421	0.0	0.45953235	3.18387	0.0	0.0582688...
U72882_s...	0.7006944	-0.031090...	-0.307484...	-0.540384...	0.11984403	2.304099	2.7795796

Restore Original Data

Undo Last Run

Run Pipeline

Delete Selected Item

Cl Pip

Data distribution

Compare two runs


Desk 0

XU col

City

ToolB

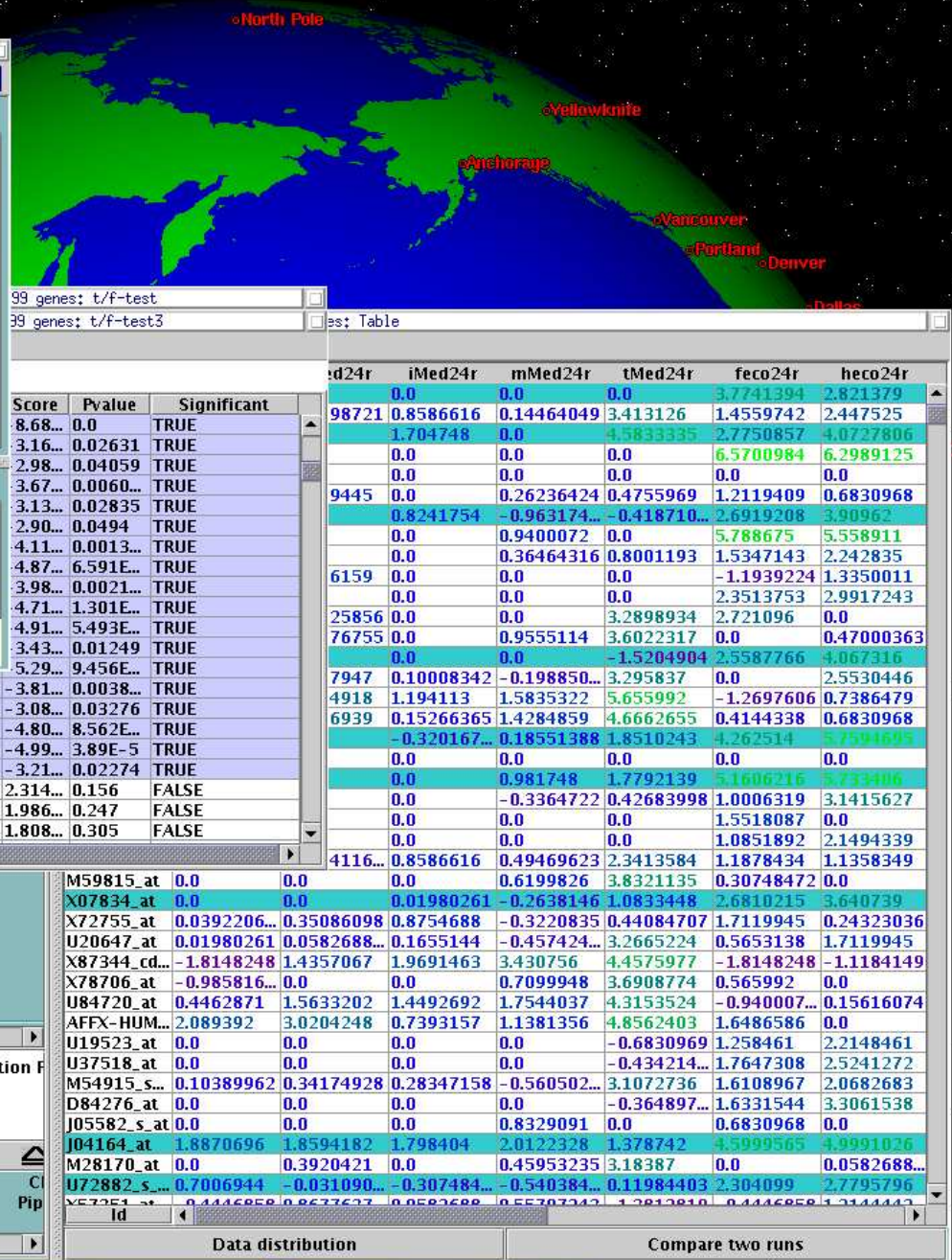
Microarray41



Rows	Columns	0.448...	-0.3077...	-0.26246506	0.351...	-3.8...
		0.417...	-0.1993...	-0.08535983	0.359...	-3.0...
Transform		0.128...	0.95818...	0.42007646	1.121...	-4.8...
Normalize		0.423...	-0.1998...	-0.20834534	0.250...	-4.9...
Clip Values		0.580...	0.5062304	0.09229204	1.056...	-3.2...
Log		1.983...	1.0105991	0.5785806	1.381...	2.31...
		3.190...	0.0	0.0	0.0	1.98...
		2.802...	0.0	0.0	0.0	1.80...
Parameters						

Please Drag and Drop Execution Units From The Operation Panel

⏪	⏮	⏭	✖	🗑
Restore Original Data	Undo Last Run	Run Pipeline	Delete Selected Item	Clear Pipeline



ToolBus

File Edit Help

Tools Views Groups

Selected Items

Microarray: 14 runs on 4199 genes (ecoli) (Microarray: 14 runs...
Microarray: 14 runs on 4199 genes (flu) (Microarray: 14 runs o...
Microarray: 14 runs on 4199 genes (yeast) (Microarray: 14 run...

New Edit Compare Remove Find

Active Tools

Tool	Status	Start	Elapsed
Statistic Analysis (T-t...	Completed	4/29/05 8:50 ...	00:00:38
Open File	Completed	4/29/05 8:36 ...	00:00:00

Stop Reuse Info Delete

Group Comparisons

File

Legend:
n: intersect
-: subtract

Reset Close

North Pole
Yellowknife
Anchorage
Vancouver
Portland
Denver
Seattle

99 genes: t/f-test
Microarray: 14 runs on 4199 genes: Table

Id	fMed24r	hMed24r	iMed24r	mMed24r	tMed24r	feco24r	heco24r
X67325_at	0.0	0.0	0.0	0.0	0.0	3.7741394	2.821379
M97936_at	0.5785806	0.05798721	0.8586616	0.14464049	3.413126	1.4559742	2.447525
HG544-HT...	0.0	0.0	1.704748	0.0	4.5833335	2.7750857	4.0727806
V00594_at	0.0	0.0	0.0	0.0	0.0	6.5700984	6.2989125
U59286_at	0.0	0.0	0.0	0.0	0.0	0.0	0.0
X02530_at	0.0	0.6729445	0.0	0.26236424	0.4755969	1.2119409	0.6830968
U52513_at	0.0	0.0	0.8241754	-0.963174...	-0.418710...	2.6919208	3.90962
X64177_f_at	0.0	0.0	0.0	0.9400072	0.0	5.788675	5.558911
M65290_at	0.0	0.0	0.0	0.36464316	0.8001193	1.5347143	2.242835
M63573_at	-1.1939224	1.5686159	0.0	0.0	0.0	-1.1939224	1.3350011
U31628_at	0.0	0.0	0.0	0.0	0.0	2.3513753	2.9917243
HG3033-H...	-0.277631...	0.90825856	0.0	0.0	3.2898934	2.721096	0.0
Y08682_rn...	0.0	0.88376755	0.0	0.9555114	3.6022317	0.0	0.47000363
M33882_at	0.0	0.0	0.0	0.0	-1.5204904	2.5587766	4.067316
U22662_at	0.0	1.4997947	0.10008342	-0.198850...	3.295837	0.0	2.5530446
S57235_at	-1.2697606	2.7474918	1.194113	1.5835322	5.655992	-1.2697606	0.7386479
AFFX-HUM...	1.708182	2.8746939	0.15266365	1.4284859	4.6662655	0.4144338	0.6830968
M13755_at	0.7613554	0.0	-0.320167...	0.18551388	1.8510243	4.262514	5.7594695
HG2724-H...	0.0	0.0	0.0	0.0	0.0	0.0	0.0
M21121_at	-0.095310...	0.0	0.0	0.981748	1.7792139	5.1606216	5.734866
M24594_at	0.0582688...	0.0	0.0	-0.3364722	0.42683998	1.0006319	3.1415627
U77180_at	0.0	0.0	0.0	0.0	0.0	1.5518087	0.0
D38128_at	0.0	0.0	0.0	0.0	0.0	1.0851892	2.1494339
AB000115...	0.59883654	-0.564116...	0.8586616	0.49469623	2.3413584	1.1878434	1.1358349
M59815_at	0.0	0.0	0.0	0.6199826	3.8321135	0.30748472	0.0
X07834_at	0.0	0.0	0.01980261	-0.2638146	1.0833448	2.6810215	3.640739
X72755_at	0.0392206...	0.35086098	0.8754688	-0.3220835	0.44084707	1.7119945	0.24323036
U20647_at	0.01980261	0.0582688...	0.1655144	-0.457424...	3.2665224	0.5653138	1.7119945
X87344_cd...	-1.8148248	1.4357067	1.9691463	3.430756	4.4575977	-1.8148248	-1.1184149
X78706_at	-0.985816...	0.0	0.0	0.7099948	3.6908774	0.565992	0.0
U84720_at	0.4462871	1.5633202	1.4492692	1.7544037	4.3153524	-0.940007...	0.15616074
AFFX-HUM...	2.089392	3.0204248	0.7393157	1.1381356	4.8562403	1.6486586	0.0
U19523_at	0.0	0.0	0.0	0.0	-0.6830969	1.258461	2.2148461
U37518_at	0.0	0.0	0.0	0.0	-0.434214...	1.7647308	2.5241272
M54915_s...	0.10389962	0.34174928	0.28347158	-0.560502...	3.1072736	1.6108967	2.0682683
D84276_at	0.0	0.0	0.0	0.0	-0.364897...	1.6331544	3.3061538
J05582_s_at	0.0	0.0	0.0	0.8329091	0.0	0.6830968	0.0
J04164_at	1.8870696	1.8594182	1.798404	2.0122328	1.378742	4.3999565	4.9991026
M28170_at	0.0	0.3920421	0.0	0.45953235	3.18387	0.0	0.0582688...
U72882_s...	0.7006944	-0.031090...	-0.307484...	-0.540384...	0.11984403	2.304099	2.7795796
X67325_at	0.4446958	0.8637637	0.8586616	0.55707342	1.3813810	0.4446958	1.3144442

Data distribution Compare two runs

Desk 0

XU CO

ToolBus
Group
Microarray: 1

ToolBus

File Edit Help

Tools Views Groups

Selected Items

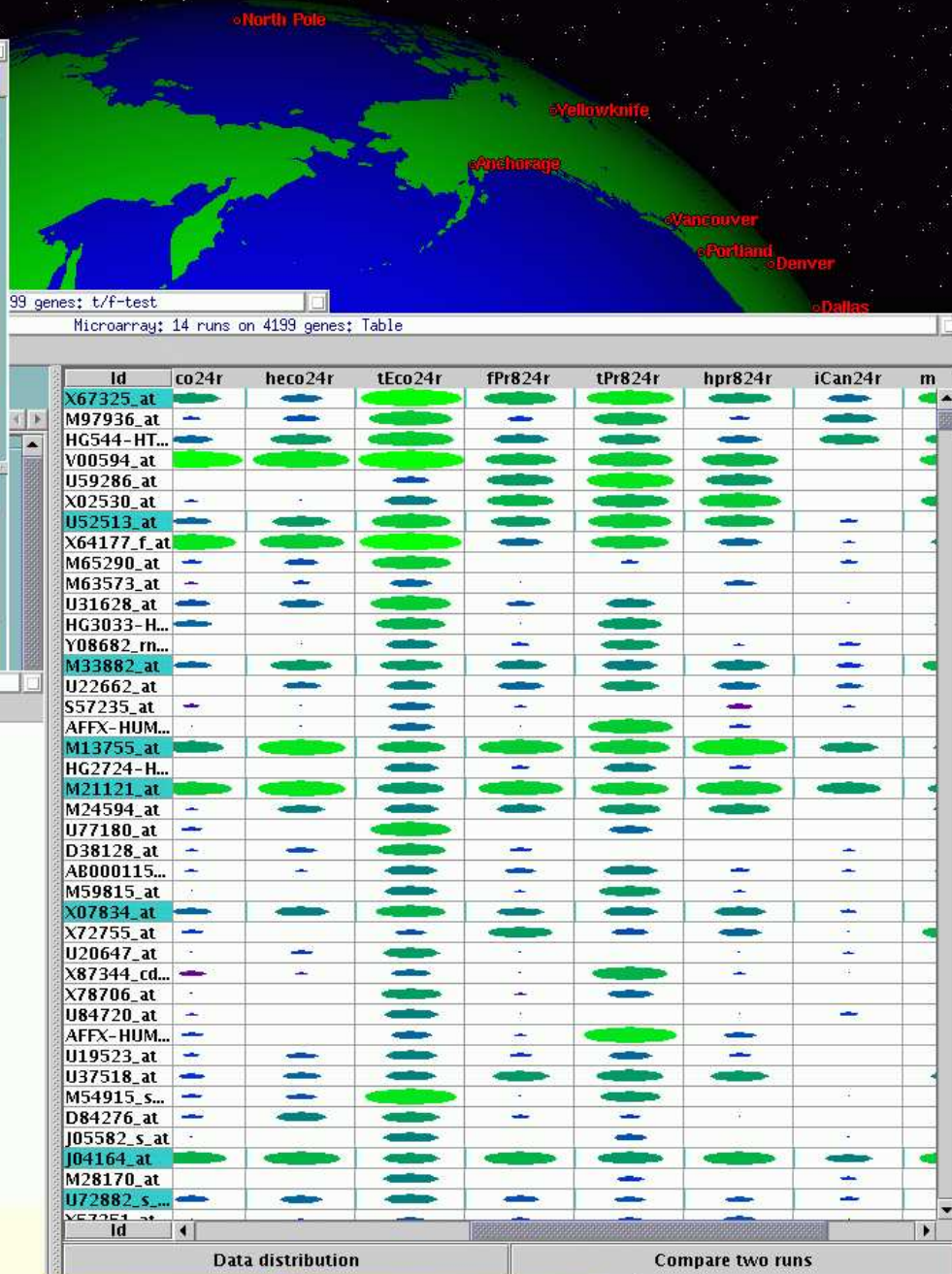
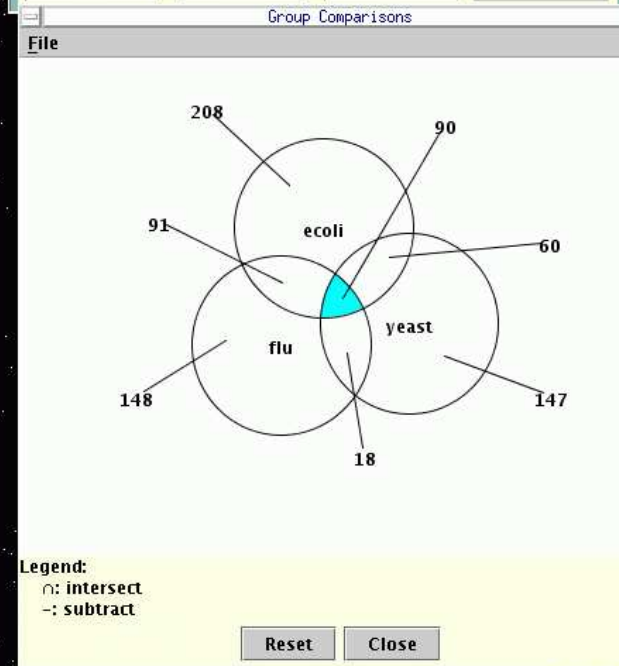
Microarray: 14 runs on 4199 genes (ecoli) (Microarray: 14 runs...
 Microarray: 14 runs on 4199 genes (flu) (Microarray: 14 runs o...
 Microarray: 14 runs on 4199 genes (yeast) (Microarray: 14 run...

New Edit Compare Remove Find

Active Tools

Tool	Status	Start	Elapsed
Statistic Analysis (T-t...	Completed	4/29/05 8:50 ...	00:00:38
Open File	Completed	4/29/05 8:36 ...	00:00:00

Stop Reuse Info Delete



Desk 0

XU co

ToolB

array: 1

Group



Want to Know More About a Pathogen?

Detailed curated information, gathered from a variety of information sources, for 21 pathogens from the CDC category A and B, and the NIAID priority category A, B, and C pathogen lists is available via a free and open XML format developed at VBI, the Pathogen Information Markup Language (PIML).



Pathogen Information (PathInfo)

[About](#) || [Pathogens](#) || [Query](#) || [TB/PP PathInfo](#) || [PIML Format](#) || [Download](#) || [Feedback](#)

► **About the PathInfo Project:** A vast amount of information about animal and plant pathogens has been acquired, stored, and displayed in varied formats through different resources, both electronic and otherwise, some accessible through the Internet. However, there is no community standard format for organizing this information, nor agreement on a machine-readable format for data exchange, thereby hampering interoperation efforts across information systems. To address this, we developed the Pathogen Information Markup Language (PIML), a free, open, XML-based format for representing pathogen information. XSLT-based visual presentations of valid PIML documents were also developed and can be accessed through a public PathInfo website or as part of the interoperating web services federation known as [ToolBus/PathPort \(TB/PP\)](#). Detailed PIML documents are available for 21 pathogens deemed of high priority with regard to public health and national biological defense. A dynamic query system allows simple queries as well as comparisons among these pathogens. Continuing efforts are being taken to include other groups' supporting PIML and create larger sets of PIML documents.

► **Pathogens available in our PathInfo Database:** All of the available 21 pathogens belong to [CDC category A or B pathogen lists](#) and/or [NIAID priority category A, B, or C pathogen lists](#). Eight of these pathogens are targets of the collaborative [MARCE](#) (Middle Atlantic Regional Center of Excellence in Biodefense and Emerging Infectious Diseases) project. Virginia Bioinformatics Institute serves as the Bioinformatics and Genomics Research Core for the entire MARCE consortium of 14 universities, diverse federal agencies and corporations.

Pathogen Information	CDC Category	NIAID Category	MARCE
<i>Bacillus anthracis</i> (Anthrax) [HTML] [PIML]	A	A	X
<i>Brucella</i> spp. (Brucellosis) [HTML] [PIML]	B	B	
<i>Burkholderia mallei</i> (Glanders) [HTML] [PIML]	B	B	
<i>Coxiella burnetii</i> (Q fever) [HTML] [PIML]	B	B	
Crimean Congo Virus [HTML] [PIML]		C	
<i>Cryptosporidium parvum</i> [HTML] [PIML]		B	X
Venezuelan Equine Encephalitis Virus [HTML]	B	B	X



PATHINFO

Pathogen Information

QUERY SYSTEM



VIRGINIA BIOINFORMATICS INSTITUTE PATHOGEN PORTAL PROJECT

◆ **PathInfo Query:** Select one or more pathogens and one topic, then click "Submit Query". The information about the specific topic related to the pathogen(s) will be extracted and displayed. To select more than one pathogen, press "Ctrl" or "Shift" button in the keyboard, hold it and click on specific pathogens.

Pathogen(s):

Bacillus anthracis
Brucella spp.
Burkholderia mallei
Crimean Congo Virus
Cryptosporidium parvum

Query Topic:

Genome Summary

Submit Query

◆ **Note:** Please go the [PathInfo cover page](#) to check the complete curated information for a specific pathogen.

Please send your feedback to us at pathinfo@vbi.vt.edu.

PATHINFO
Pathogen Information**QUERY
SYSTEM**

VIRGINIA BIOINFORMATICS INSTITUTE PATHOGEN PORTAL PROJECT



◆ **PathInfo Query:** Select one or more pathogens and one topic, then click "Submit Query". The information about the specific topic related to the pathogen(s) will be extracted and displayed. To select more than one pathogen, press "Ctrl" or "Shift" button in the keyboard, hold it and click on specific pathogens.

Pathogen(s):

Junin Virus
Lassa Virus
Machupo Virus
Marburg Virus
Rift Valley Fever Virus

Query Topic:

Symptoms

Submit Query

◆ **Note:** Please go the [PathInfo cover page](#) to check the complete curated information for a specific pathogen.

Please send your feedback to us at pathinfo@vbi.vt.edu.

Query Topic: Disease Symptoms

Ebola Virus

A. Human -- Disease Symptom Information:

a. Symptom Information of Ebola (i.e., Ebola hemorrhagic fever) :

• Syndrome -- Viral Hemorrhagic Fever

- **Description:** The term viral hemorrhagic fever (VHF) refers to the illness associated with a number of geographically restricted viruses. This illness is characterized by fever and, in the most severe cases, shock and hemorrhage. Although a number of other febrile viral infections may produce hemorrhage, only the agents of Lassa, Marburg, Ebola, and Crimean-Congo hemorrhagic fevers are known to have caused significant outbreaks of disease with person-to-person transmission. ([MMWR, 1988](#))
- **Observed:** The illness-to-infection ratio for Ebola virus is unknown, but seroepidemiologic investigations suggest that mild or asymptomatic infections can occur. ([MMWR, 1988](#))
- **Specific Symptoms:**
 - **Ebola Hemorrhagic Fever**
 - **Description:** The onset of illness is abrupt, and initial symptoms resemble those of an influenza-like syndrome. Fever, headache, general malaise, myalgia, joint pain, and sore throat are commonly followed by diarrhea and abdominal pain. A transient morbilliform skin rash, which subsequently desquamates, often appears at the end of the first week of illness. Other physical findings include pharyngitis, which is frequently exudative, and occasionally conjunctivitis, jaundice, and edema. After the third day of illness, hemorrhagic manifestations are common and include petechiae as well as frank bleeding, which

Marburg Virus

A. Human -- Disease Symptom Information:

a. Symptom Information of Marburg (i.e., Marburg hemorrhagic fever) :

• Syndrome -- Viral Hemorrhagic Fever

- **Description:** The term viral hemorrhagic fever (VHF) refers to the illness associated with a number of geographically restricted viruses. This illness is characterized by fever and, in the most severe cases, shock and hemorrhage. Although a number of other febrile viral infections may produce hemorrhage, only the agents of Lassa, Marburg, Ebola, and Crimean-Congo hemorrhagic fevers are known to have caused significant outbreaks of disease with person-to-person transmission. ([MMWR, 1988](#)) The onset of illness is abrupt, and initial symptoms resemble those of an influenza-like syndrome. Fever, headache, general malaise, myalgia, joint pain, and sore throat are commonly followed by diarrhea and abdominal pain. A transient morbilliform skin rash, which subsequently desquamates, often appears at the end of the first week of illness. Other physical findings include pharyngitis, which is frequently exudative, and occasionally conjunctivitis, jaundice, and edema. After the third day of illness, hemorrhagic manifestations are common and include petechiae as well as frank bleeding, which can arise from any part of the gastrointestinal tract and from multiple other sites. ([MMWR, 1988](#))
- **Observed:** Marburg hemorrhagic fever is a very rare human disease. ([Website 8](#))
- **Ebola-like symptoms**
 - **Description:** Clinical and laboratory features of Marburg virus disease are essentially similar to those describe for Ebola virus disease. ([MMWR, 1988](#))



Bacillus anthracis

Contents:

Organism

- A. Taxonomy
- B. Lifecycle
- C. Genome Summary

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- A. Outbreak Locations
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Infected Hosts

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- 2. Infection Process
- 3. Disease Information
- 4. Prevention
- 5. Model System

B. Grazing Herbivores

- 1. Taxonomy
- 2. Infection Process
- 3. Disease Information
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C. Laboratory Model Animals

- 1. Taxonomy
- 2. Infection Process
- 3. Disease Information
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- 5. Model System

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- A. Biosafety Information
- B. Culturing Information
- C. Diagnostic Tests

- 1. Organism Detection
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- 3. Nucleic Acid Detection
- 4. Other Tests

References

- A. Journal References
- B. Book References
- C. Website References

Bacillus anthracis

I. Organism Information

A. Taxonomy Information

1. Species:

- a. *Bacillus anthracis* ([Shafazand et al., 1999](#), [Website 15](#)):

- i. GenBank Taxonomy No.: [1392](#)

- ii. **Description:** The anthrax bacterium is named *Bacillus anthracis* because it is rod-shaped when viewed under a microscope. The name "Bacillus" comes from the Latin word "baculus," meaning "rod." Anthrax is derived from the Greek word for coal, the characteristic color and appearance of the eschar in cutaneous anthrax. Anthrax is also known as charbon (pronounced shar-bawn), which is French for coal. Pulmonary anthrax is also known as woolsorter's disease. This is because people who sorted the wool of animals had contracted it in this way ([Shafazand et al., 1999](#)).

iii. Variant(s):

- **Ames Strain** ([Cummings et al., 2002](#), [Read et al., 2002](#)):

- **Parent:** *Bacillus anthracis*

- **Description:** The *Bacillus anthracis* Ames strain, is highly virulent and contains pXO1 and pXO2 plasmids. It was originally isolated from a dead cow in Texas in 1981. The geographic region for this strain is the United States of America and the United Kingdom. Sequencing of the genomes of two isolates have been completed ([Website 14](#), [Cummings et al., 2002](#), [Website 32](#), [Website 33](#)).

- **Porton Strain of Ames isolate** ([Cummings et al., 2002](#), [Read et al., 2002](#)):

- **Parent:** [Ames Strain](#)

- **Description:** The *Bacillus anthracis* Porton Ames isolate (pXO1-, pXO2-) was sequenced at the Institute for Genomic Research in 1999-2003 ([Website 32](#)).

- **Florida isolate of Ames Strain** ([Cummings et al., 2002](#), [Read et al., 2002](#)):

- **Parent:** [Ames Strain](#)

- **Description:** The whole genome of *Bacillus anthracis* strain A2012, the Florida isolate has been sequenced. This isolate was from a victim of a recent bioterrorist anthrax attack ([website 17](#), [Website 33](#), [Read et al., 2002](#)).

- **Pasteur Strain** ([Read et al., 2002](#)):

- **Parent:** *Bacillus anthracis*

- **Sterne Strain** ([Cummings et al., 2002](#), [Read et al., 2002](#)):

- **Description:** Recently, using multiple-locus variable number tandem repeat (VNTR) analysis bioterror strain was identified as the veterinary vaccine strain, Sterne 34F2. Geographic region is in China. Sequencing is being considered and may be sequenced in the future ([Cummings et al., 2002](#)).

- **Strain 01-282C-1** ([Cummings et al., 2002](#)):

V. References

A. Journal References:

Ahuja et al., 2001: Ahuja N., Kumar P., Bhatnagar R. Hydrophobic Residues Phe552, Phe554, Ile562, Leu566, and Ile574 are required for Oligomerization of Anthrax Protective Antigen. *Biochemical and Biophysical Research Communications*. 2001; 287(2): 542 - 549. [PubMed: [11554763](#)].

Andrews et al., 2002: Andrews L.M., Wise D. Susceptibility testing of *Bacillus* species. *J. Antimicrob. Chemother.* 2002;



Bacillus anthracis

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B. Grazing Herbivores

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References

- A. [Journal References](#)
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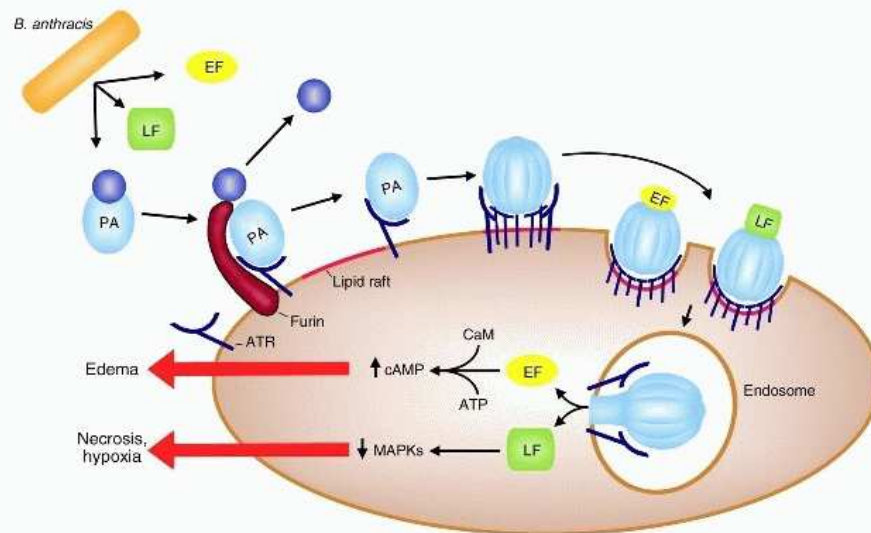
([website 2](#), [website 7](#)).

3. Disease Information:

a. Cutaneous anthrax ([Website 2](#)):

- i. **Pathogenesis Mechanism:** Disease results when *Bacillus anthracis* spores are introduced into the skin via inoculation of small cuts/abrasions or inapparent skin lesions. Endospores often are phagocytosed by macrophages and carried to regional lymph nodes, causing painful lymphadenopathy and lymphangitis. Low-level germination at the site of introduction leads to localized necrosis with eschar formation and soft-tissue or mucosal edema (which can be massive in some cases). Hematogenous spread with resultant toxemia can occur, although such spread is not common with appropriate antibiotic therapy ([Website 7](#), [Website 2](#)).

■ Pathogenesis of *B. anthracis* ([Prince, 2003](#)):



Description: How anthrax toxins cause pathology. Fully virulent *B. anthracis* produce an antiphagocytic capsule as well as toxins. The protective antigen (PA) of the anthrax toxin binds to the ATR on the host cell surface. The 83-kDa form of PA is cleaved by the cell surface protease furin and produces a 63-kDa monomer. Heptamerization of PA induces clustering of the ATRs, association of the complex with lipid rafts, and exposure of binding domains to the edema factor (EF) or the lethal factor (LF). The heptamer, and bound EF or LF, are then endocytosed. EF, an adenylate cyclase, and LF, a Zn²⁺ metalloprotease, translocate to the cytosol through a pore

V. References

A. Journal References:

Ahuja et al., 2001: Ahuja N., Kumar P., Bhatnagar R. Hydrophobic Residues Phe552, Phe554, Ile562, Leu566, and Ile574 are required for Oligomerization of Anthrax Protective Antigen. *Biochemical and Biophysical Research Communications*. 2001; 287(2): 542 - 549. [PubMed: [11554763](#)].

Andrews et al., 2002: Andrews L.M., Wise D. Susceptibility testing of *Bacillus* species. *J. Antimicrob. Chemother.* 2002;

PATHPORT

The pathogen portal project

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[VBI](#)

PathPort, short for pathogen portal, combines information about pathogens (and their near relatives) from around the world with powerful analysis and visualization tools to aid in the rapid detection, identification, and forensic attribution of high-priority pathogens, whether causing infectious diseases or potentially used as a biological weapons.

To provide this platform, VBI will perform genome data acquisition, vetting, consolidation, and annotation; create the data model, graphical user interface, bioinformatics tools for analysis, and the portal; develop methods to validate candidate target sequences; and research host response to pathogen models.

The software infrastructure supporting the PathPort project is built around ToolBus, a client-side interconnect. ToolBus allows researchers to easily access web-services from all over the world (as well as programs and files on their desktop computer), which provide both data and analysis services, and to examine the results using a wide variety of visualization tools. In addition, ToolBus enables users to form groupings of related information and to perform comparative analysis using these data groups in order to support the discovery of interesting inter-data relationships.

ToolBus is a general purpose client-side interconnect and is not in any way tied to a particular domain. Rather, it is the collection of web-services, such as those for gene prediction and multiple sequence alignment, along with visualization tools for viewing this kind of information that turns the collection of components into PathPort.

News

[Web Services Symposium](#)[PathPort/ToolBus Version 2.0 Released](#)[PathPort training on the road](#)[PathPort/ToolBus Version 1.1 Released](#)[Older News ...](#)*Last modified on 29Apr2005**pathport@vbi.vt.edu*

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